

| | | | | | |
|-----|----|-----|------|---------|-----------|
| 18 | 17 | MAR | 2000 | 2000005 | 1961.743P |
| 19 | 18 | APR | 2000 | 2000005 | 1961.243P |
| 20 | 19 | MAY | 2000 | 2000005 | 2075.153P |
| 21 | 20 | JUN | 2000 | 2000005 | 2074.673P |
| 22 | 21 | JUN | 2000 | 2000005 | 2174.886P |
| 23 | 22 | JUN | 2000 | 2000005 | 2174.153P |
| 24 | 23 | JUL | 2000 | 2000005 | 2166.473P |
| 25 | 24 | JUL | 2000 | 2000005 | 2168.003P |
| 26 | 25 | JUL | 2000 | 2000005 | 2174.873P |
| 27 | 26 | AUG | 2000 | 2000005 | 2174.964P |
| 28 | 27 | AUG | 2000 | 2000005 | 2275.254P |
| 29 | 28 | AUG | 2000 | 2000005 | 2275.254P |
| 30 | 29 | AUG | 2000 | 2000005 | 2275.254P |
| 31 | 30 | AUG | 2000 | 2000005 | 2275.254P |
| 32 | 31 | AUG | 2000 | 2000005 | 2275.254P |
| 33 | 32 | AUG | 2000 | 2000005 | 2275.254P |
| 34 | 33 | AUG | 2000 | 2000005 | 2275.254P |
| 35 | 34 | AUG | 2000 | 2000005 | 2275.254P |
| 36 | 35 | AUG | 2000 | 2000005 | 2275.254P |
| 37 | 36 | AUG | 2000 | 2000005 | 2275.254P |
| 38 | 37 | AUG | 2000 | 2000005 | 2275.254P |
| 39 | 38 | AUG | 2000 | 2000005 | 2275.254P |
| 40 | 39 | AUG | 2000 | 2000005 | 2275.254P |
| 41 | 40 | AUG | 2000 | 2000005 | 2275.254P |
| 42 | 41 | AUG | 2000 | 2000005 | 2275.254P |
| 43 | 42 | AUG | 2000 | 2000005 | 2275.254P |
| 44 | 43 | AUG | 2000 | 2000005 | 2275.254P |
| 45 | 44 | AUG | 2000 | 2000005 | 2275.254P |
| 46 | 45 | AUG | 2000 | 2000005 | 2275.254P |
| 47 | 46 | AUG | 2000 | 2000005 | 2275.254P |
| 48 | 47 | AUG | 2000 | 2000005 | 2275.254P |
| 49 | 48 | AUG | 2000 | 2000005 | 2275.254P |
| 50 | 49 | AUG | 2000 | 2000005 | 2275.254P |
| 51 | 50 | AUG | 2000 | 2000005 | 2275.254P |
| 52 | 51 | AUG | 2000 | 2000005 | 2275.254P |
| 53 | 52 | AUG | 2000 | 2000005 | 2275.254P |
| 54 | 53 | AUG | 2000 | 2000005 | 2275.254P |
| 55 | 54 | AUG | 2000 | 2000005 | 2275.254P |
| 56 | 55 | AUG | 2000 | 2000005 | 2275.254P |
| 57 | 56 | AUG | 2000 | 2000005 | 2275.254P |
| 58 | 57 | AUG | 2000 | 2000005 | 2275.254P |
| 59 | 58 | AUG | 2000 | 2000005 | 2275.254P |
| 60 | 59 | AUG | 2000 | 2000005 | 2275.254P |
| 61 | 60 | AUG | 2000 | 2000005 | 2275.254P |
| 62 | 61 | AUG | 2000 | 2000005 | 2275.254P |
| 63 | 62 | AUG | 2000 | 2000005 | 2275.254P |
| 64 | 63 | AUG | 2000 | 2000005 | 2275.254P |
| 65 | 64 | AUG | 2000 | 2000005 | 2275.254P |
| 66 | 65 | AUG | 2000 | 2000005 | 2275.254P |
| 67 | 66 | AUG | 2000 | 2000005 | 2275.254P |
| 68 | 67 | AUG | 2000 | 2000005 | 2275.254P |
| 69 | 68 | AUG | 2000 | 2000005 | 2275.254P |
| 70 | 69 | AUG | 2000 | 2000005 | 2275.254P |
| 71 | 70 | AUG | 2000 | 2000005 | 2275.254P |
| 72 | 71 | AUG | 2000 | 2000005 | 2275.254P |
| 73 | 72 | AUG | 2000 | 2000005 | 2275.254P |
| 74 | 73 | AUG | 2000 | 2000005 | 2275.254P |
| 75 | 74 | AUG | 2000 | 2000005 | 2275.254P |
| 76 | 75 | AUG | 2000 | 2000005 | 2275.254P |
| 77 | 76 | AUG | 2000 | 2000005 | 2275.254P |
| 78 | 77 | AUG | 2000 | 2000005 | 2275.254P |
| 79 | 78 | AUG | 2000 | 2000005 | 2275.254P |
| 80 | 79 | AUG | 2000 | 2000005 | 2275.254P |
| 81 | 80 | AUG | 2000 | 2000005 | 2275.254P |
| 82 | 81 | AUG | 2000 | 2000005 | 2275.254P |
| 83 | 82 | AUG | 2000 | 2000005 | 2275.254P |
| 84 | 83 | AUG | 2000 | 2000005 | 2275.254P |
| 85 | 84 | AUG | 2000 | 2000005 | 2275.254P |
| 86 | 85 | AUG | 2000 | 2000005 | 2275.254P |
| 87 | 86 | AUG | 2000 | 2000005 | 2275.254P |
| 88 | 87 | AUG | 2000 | 2000005 | 2275.254P |
| 89 | 88 | AUG | 2000 | 2000005 | 2275.254P |
| 90 | 89 | AUG | 2000 | 2000005 | 2275.254P |
| 91 | 90 | AUG | 2000 | 2000005 | 2275.254P |
| 92 | 91 | AUG | 2000 | 2000005 | 2275.254P |
| 93 | 92 | AUG | 2000 | 2000005 | 2275.254P |
| 94 | 93 | AUG | 2000 | 2000005 | 2275.254P |
| 95 | 94 | AUG | 2000 | 2000005 | 2275.254P |
| 96 | 95 | AUG | 2000 | 2000005 | 2275.254P |
| 97 | 96 | AUG | 2000 | 2000005 | 2275.254P |
| 98 | 97 | AUG | 2000 | 2000005 | 2275.254P |
| 99 | 98 | AUG | 2000 | 2000005 | 2275.254P |
| 100 | 99 | AUG | 2000 | 2000005 | 2275.254P |

[illegible]

Genetic version 5.1.3
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09 nucleotide multiple search, using SW model

from cut: February 1, 2003, 23:50:15 : Search time 2098 seconds

(without alignments)

#872,723 Million cell updates/sec

1 hit: 98.09 875.076-19

Footprint score: 11.22

Sequence: 1 atggcaaacatgccatataa.....aacctccatcatatata 1122

Search table: MEMBLITY.M0

Gapop 10.0, Gapext 1.0

Searched: 16,540,066 seqs, 8097748376 residues

Total number of hits satisfying chosen parameters: 42,00132

Minimum hit seq length: 0

Maximum hit seq length: 200000000

Foot processing: Minimum Match 48

Justified first 45 summaries

EST:*

1: cm_estb1.*

2: cm_estb2.*

3: cm_estb3.*

4: cm_estb4.*

5: cm_estb5.*

6: cm_estb6.*

7: cm_estb7.*

8: cm_estb8.*

9: cm_estb9.*

10: cm_estb10.*

11: cm_estb11.*

12: cm_estb12.*

13: cm_estb13.*

14: cm_estb14.*

15: cm_estb15.*

16: cm_estb16.*

17: cm_estb17.*

18: cm_estb18.*

19: cm_estb19.*

20: cm_estb20.*

21: cm_estb21.*

22: cm_estb22.*

23: cm_estb23.*

Foot. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARY

| Result | No. | Score | Query | Match | Length | DB | CD | Description |
|--------|-------|-------|-------|-------|----------|-------------------|----|-------------|
| 1 | 662.8 | 60.8 | 958 | 14 | 6115794 | 602866250 | | |
| 2 | 56.4 | 59.2 | 726 | 14 | 61602566 | 603248985 | | |
| 3 | 53.8 | 47.4 | 577 | 14 | 60257512 | 621158 MA | | |
| 4 | 52.8 | 46.7 | 996 | 17 | 60257512 | 621158 MA | | |
| 5 | 51.4 | 45.9 | 727 | 14 | 60951848 | 60951848 01 M EHO | | |
| 6 | 51.2 | 45.7 | 726 | 14 | 60951848 | 60951848 01 M EHO | | |

| | | | | | | | | |
|---|----|-------|------|------|----|----------|----------|--------------|
| c | 7 | 508.2 | 45.4 | 1000 | 17 | CNS03028 | At2g2727 | 1013 Arabid. |
| c | 8 | 491.8 | 43.8 | 1013 | 17 | CNS03028 | At2g2727 | 1013 Arabid. |
| c | 9 | 465.4 | 41.5 | 2105 | 17 | CNS03028 | At2g2727 | 1013 Arabid. |
| c | 10 | 444.6 | 39.6 | 817 | 17 | CNS03028 | At2g2727 | 1013 Arabid. |
| c | 11 | 437.2 | 35.8 | 980 | 17 | CNS03028 | At2g2727 | 1013 Arabid. |
| c | 12 | 464.6 | 42.5 | 570 | 17 | CNS03028 | At2g2727 | 1013 Arabid. |
| c | 13 | 441 | 40.4 | 818 | 17 | CNS03028 | At2g2727 | 1013 Arabid. |
| c | 14 | 448.4 | 40.2 | 602 | 17 | CNS03028 | At2g2727 | 1013 Arabid. |
| c | 15 | 446.6 | 40.0 | 599 | 17 | CNS03028 | At2g2727 | 1013 Arabid. |
| c | 16 | 427.2 | 39.2 | 746 | 17 | CNS03028 | At2g2727 | 1013 Arabid. |
| c | 17 | 410.6 | 29.2 | 568 | 17 | CNS03028 | At2g2727 | 1013 Arabid. |
| c | 18 | 408.4 | 27.5 | 552 | 17 | CNS03028 | At2g2727 | 1013 Arabid. |
| c | 19 | 390.8 | 25.9 | 785 | 17 | CNS03028 | At2g2727 | 1013 Arabid. |
| c | 20 | 384.2 | 25.3 | 644 | 17 | CNS03028 | At2g2727 | 1013 Arabid. |
| c | 21 | 383.4 | 25.3 | 448 | 17 | CNS03028 | At2g2727 | 1013 Arabid. |
| c | 22 | 380.8 | 25.0 | 450 | 17 | CNS03028 | At2g2727 | 1013 Arabid. |
| c | 23 | 277.8 | 24.8 | 521 | 17 | CNS03028 | At2g2727 | 1013 Arabid. |
| c | 24 | 276 | 24.6 | 646 | 17 | CNS03028 | At2g2727 | 1013 Arabid. |
| c | 25 | 270.4 | 24.1 | 944 | 17 | CNS03028 | At2g2727 | 1013 Arabid. |
| c | 26 | 269.8 | 24.0 | 1052 | 17 | CNS03028 | At2g2727 | 1013 Arabid. |
| c | 27 | 260.9 | 23.2 | 605 | 17 | CNS03028 | At2g2727 | 1013 Arabid. |
| c | 28 | 242 | 21.6 | 648 | 17 | CNS03028 | At2g2727 | 1013 Arabid. |
| c | 29 | 226.2 | 20.2 | 690 | 17 | CNS03028 | At2g2727 | 1013 Arabid. |
| c | 30 | 221.6 | 19.8 | 986 | 17 | CNS03028 | At2g2727 | 1013 Arabid. |
| c | 31 | 198.8 | 17.7 | 767 | 17 | CNS03028 | At2g2727 | 1013 Arabid. |
| c | 32 | 192.6 | 17.2 | 599 | 17 | CNS03028 | At2g2727 | 1013 Arabid. |
| c | 33 | 190.8 | 17.0 | 461 | 17 | CNS03028 | At2g2727 | 1013 Arabid. |
| c | 34 | 189.6 | 16.9 | 216 | 17 | CNS03028 | At2g2727 | 1013 Arabid. |
| c | 35 | 184.6 | 16.5 | 676 | 17 | CNS03028 | At2g2727 | 1013 Arabid. |
| c | 36 | 178.4 | 15.9 | 547 | 17 | CNS03028 | At2g2727 | 1013 Arabid. |
| c | 37 | 172.4 | 15.4 | 806 | 17 | CNS03028 | At2g2727 | 1013 Arabid. |
| c | 38 | 170.4 | 15.2 | 414 | 17 | CNS03028 | At2g2727 | 1013 Arabid. |
| c | 39 | 168.8 | 15.0 | 427 | 17 | CNS03028 | At2g2727 | 1013 Arabid. |
| c | 40 | 168.8 | 15.0 | 444 | 17 | CNS03028 | At2g2727 | 1013 Arabid. |
| c | 41 | 167.8 | 15.0 | 548 | 17 | CNS03028 | At2g2727 | 1013 Arabid. |
| c | 42 | 162.6 | 14.5 | 409 | 17 | CNS03028 | At2g2727 | 1013 Arabid. |
| c | 43 | 157.6 | 14.0 | 402 | 17 | CNS03028 | At2g2727 | 1013 Arabid. |
| c | 44 | 156.8 | 14.0 | 447 | 17 | CNS03028 | At2g2727 | 1013 Arabid. |
| c | 45 | 156.6 | 14.0 | 400 | 17 | CNS03028 | At2g2727 | 1013 Arabid. |

ALIGNMENTS

| | | | | | |
|--------------|--|-----------|------|--------|------------------|
| RESULT: | 6115794 | 958 bp | mRNA | Length | EST: 25 JUN 2001 |
| DEFINITION: | 602866250[1] NIH_MGC_7 Homo sapiens cDNA clone IMAGE501472.1 | | | | |
| KEYWORDS: | EST | | | | |
| VERSION: | 6115794.1 | 6115794.1 | | | |
| KEYWORDS: | EST | | | | |
| ORGANISM: | Homo sapiens | | | | |
| REFERENCE: | 1 (bases 1 to 958) | | | | |
| FEATURES: | NIH-MGC: http://mimc.nhlbi.nih.gov/ | | | | |
| DESCRIPTION: | National Institutes of Health, Mammalian Gene Collection (MGC) | | | | |
| COMMENT: | Contact: Robert Stansbury, Ph.D. | | | | |
| REFERENCE: | 1 (bases 1 to 958) | | | | |
| FEATURES: | NIH-MGC: http://mimc.nhlbi.nih.gov/ | | | | |
| DESCRIPTION: | National Institutes of Health, Mammalian Gene Collection (MGC) | | | | |
| COMMENT: | Contact: Robert Stansbury, Ph.D. | | | | |
| REFERENCE: | 1 (bases 1 to 958) | | | | |
| FEATURES: | NIH-MGC: http://mimc.nhlbi.nih.gov/ | | | | |
| DESCRIPTION: | National Institutes of Health, Mammalian Gene Collection (MGC) | | | | |
| COMMENT: | Contact: Robert Stansbury, Ph.D. | | | | |

| Index | Matrices | Size | Storage | Index | Length |
|-------|-----------------|---------|--------------------|----------|---------------|
| 00 | Identity Matrix | 100,000 | Storage: 1,992,704 | 00, 01 | Length: 3,732 |
| 01 | Lower Symmetry | 100,000 | Storage: 1,992,704 | 02, 03 | Length: 3,732 |
| 02 | MatChes | 4,732 | MatChes: 100,000 | 04, 05 | Length: 3,732 |
| 03 | MatChes | 4,732 | MatChes: 100,000 | 06, 07 | Length: 3,732 |
| 04 | MatChes | 4,732 | MatChes: 100,000 | 08, 09 | Length: 3,732 |
| 05 | MatChes | 4,732 | MatChes: 100,000 | 10, 11 | Length: 3,732 |
| 06 | MatChes | 4,732 | MatChes: 100,000 | 12, 13 | Length: 3,732 |
| 07 | MatChes | 4,732 | MatChes: 100,000 | 14, 15 | Length: 3,732 |
| 08 | MatChes | 4,732 | MatChes: 100,000 | 16, 17 | Length: 3,732 |
| 09 | MatChes | 4,732 | MatChes: 100,000 | 18, 19 | Length: 3,732 |
| 10 | MatChes | 4,732 | MatChes: 100,000 | 20, 21 | Length: 3,732 |
| 11 | MatChes | 4,732 | MatChes: 100,000 | 22, 23 | Length: 3,732 |
| 12 | MatChes | 4,732 | MatChes: 100,000 | 24, 25 | Length: 3,732 |
| 13 | MatChes | 4,732 | MatChes: 100,000 | 26, 27 | Length: 3,732 |
| 14 | MatChes | 4,732 | MatChes: 100,000 | 28, 29 | Length: 3,732 |
| 15 | MatChes | 4,732 | MatChes: 100,000 | 30, 31 | Length: 3,732 |
| 16 | MatChes | 4,732 | MatChes: 100,000 | 32, 33 | Length: 3,732 |
| 17 | MatChes | 4,732 | MatChes: 100,000 | 34, 35 | Length: 3,732 |
| 18 | MatChes | 4,732 | MatChes: 100,000 | 36, 37 | Length: 3,732 |
| 19 | MatChes | 4,732 | MatChes: 100,000 | 38, 39 | Length: 3,732 |
| 20 | MatChes | 4,732 | MatChes: 100,000 | 40, 41 | Length: 3,732 |
| 21 | MatChes | 4,732 | MatChes: 100,000 | 42, 43 | Length: 3,732 |
| 22 | MatChes | 4,732 | MatChes: 100,000 | 44, 45 | Length: 3,732 |
| 23 | MatChes | 4,732 | MatChes: 100,000 | 46, 47 | Length: 3,732 |
| 24 | MatChes | 4,732 | MatChes: 100,000 | 48, 49 | Length: 3,732 |
| 25 | MatChes | 4,732 | MatChes: 100,000 | 50, 51 | Length: 3,732 |
| 26 | MatChes | 4,732 | MatChes: 100,000 | 52, 53 | Length: 3,732 |
| 27 | MatChes | 4,732 | MatChes: 100,000 | 54, 55 | Length: 3,732 |
| 28 | MatChes | 4,732 | MatChes: 100,000 | 56, 57 | Length: 3,732 |
| 29 | MatChes | 4,732 | MatChes: 100,000 | 58, 59 | Length: 3,732 |
| 30 | MatChes | 4,732 | MatChes: 100,000 | 60, 61 | Length: 3,732 |
| 31 | MatChes | 4,732 | MatChes: 100,000 | 62, 63 | Length: 3,732 |
| 32 | MatChes | 4,732 | MatChes: 100,000 | 64, 65 | Length: 3,732 |
| 33 | MatChes | 4,732 | MatChes: 100,000 | 66, 67 | Length: 3,732 |
| 34 | MatChes | 4,732 | MatChes: 100,000 | 68, 69 | Length: 3,732 |
| 35 | MatChes | 4,732 | MatChes: 100,000 | 70, 71 | Length: 3,732 |
| 36 | MatChes | 4,732 | MatChes: 100,000 | 72, 73 | Length: 3,732 |
| 37 | MatChes | 4,732 | MatChes: 100,000 | 74, 75 | Length: 3,732 |
| 38 | MatChes | 4,732 | MatChes: 100,000 | 76, 77 | Length: 3,732 |
| 39 | MatChes | 4,732 | MatChes: 100,000 | 78, 79 | Length: 3,732 |
| 40 | MatChes | 4,732 | MatChes: 100,000 | 80, 81 | Length: 3,732 |
| 41 | MatChes | 4,732 | MatChes: 100,000 | 82, 83 | Length: 3,732 |
| 42 | MatChes | 4,732 | MatChes: 100,000 | 84, 85 | Length: 3,732 |
| 43 | MatChes | 4,732 | MatChes: 100,000 | 86, 87 | Length: 3,732 |
| 44 | MatChes | 4,732 | MatChes: 100,000 | 88, 89 | Length: 3,732 |
| 45 | MatChes | 4,732 | MatChes: 100,000 | 90, 91 | Length: 3,732 |
| 46 | MatChes | 4,732 | MatChes: 100,000 | 92, 93 | Length: 3,732 |
| 47 | MatChes | 4,732 | MatChes: 100,000 | 94, 95 | Length: 3,732 |
| 48 | MatChes | 4,732 | MatChes: 100,000 | 96, 97 | Length: 3,732 |
| 49 | MatChes | 4,732 | MatChes: 100,000 | 98, 99 | Length: 3,732 |
| 50 | MatChes | 4,732 | MatChes: 100,000 | 100, 101 | Length: 3,732 |

| | |
|----|---|
| XX | RES01.3 |
| XX | AAV065.4 |
| XX | 10 AAV065.44 standard; Protein: 47.8 AA. |
| XX | |
| XX | AAV405.44; |
| XX | |
| XX | 15-Nov 1997 (first entry) |
| XX | |
| XX | A G protein-coupled receptor protein designated SKBR3. |
| XX | |
| XX | 5. G protein-coupled receptor protein: SKBR3; central nervous system; inflammatory disorder; immunological. |
| XX | |
| XX | Human sapitens. |
| XX | |
| XX | W09046.478-A1. |
| XX | |
| XX | 16-SEP 1997. |
| XX | |
| XX | 11-MAR 1997; 93WO-440191. |
| XX | |
| XX | 12-MAR 1997; 98JP-0050245. |
| XX | 03-FEB 1997; 99JP-0026774. |
| XX | |
| XX | (YAMA) YAMANOUCHI PHARM CO. LTD. |
| XX | |
| XX | Matsuno M, Shimoto T, Takasaki J, Saito T, Kamohara M; |
| XX | |
| XX | WPT: 1999 951.407/46. |
| XX | |
| XX | N FSHB; AAV10562. |
| XX | |
| XX | G protein-coupled receptor proteins expressed in the central nervous |
| XX | system and genes encoding them - |
| XX | |
| XX | Example 1: Page 57-58; 74pp; Japanese. |
| XX | |
| XX | The present sequence represents a G protein-coupled receptor protein |
| XX | designated SKBR3. The protein is expressed in the central nervous |
| XX | system. The SKBR3 products are used for the diagnosis and treatment |

| Seq | Sequence | 473 AA: | 99.7%: Score: 1986; DB: 20; Length: 473. | Post Local Similarity: 99.7%; Prod. No.: 4,86-217; | Matches: 372; Conservation: 0; Missed: 1; Indels: 0; gaps: 0 |
|----------|--|---------|--|--|--|
| QY | 1 MANTIGEEVNSGALSPASAVKRLVILGLMVSLSGNALLSLVLERKALIRKAYE | 60 | | | |
| Lab | 1 MANTIGEEVNSGALSPASAVKRLVILGLMVSLSGNALLSLVLERKALIRKAYE | 60 | | | |
| QY | 61 LLDPLADPTISAVPEVVLASVKRHSNMTSALSCKIVAMVAPETIDAMITVSVL | 120 | | | |
| Db | 61 LLDPLADPTISAVPEVVLASVKRHSNMTSALSCKIVAMVAPETIDAMITVSVL | 120 | | | |
| QY | 121 RYMAIAHREFAKRRKRLMTCNAVTCGMATLSVMAAPPEVFNQYKREHEEQYIEHRY | 180 | | | |
| Db | 121 RYMAIAHREFAKRRKRLMTCNAVTCGMATLSVMAAPPEVFNQYKREHEEQYIEHRY | 180 | | | |
| QY | 181 EKANTLISPMILAVLRAATHAVYGRLLFEYHRKRRPVQMPATSONMTPEHDAICQ | 240 | | | |
| Db | 181 EKANTLISPMILAVLRAATHAVYGRLLFEYHRKRRPVQMPATSONMTPEHDAICQ | 240 | | | |
| QY | 241 AAANNIAPGGRPPPTLLGTRGNHAASTRLLSMPEKGRKQDRRPVATLLPLIKS | 300 | | | |
| Db | 241 AAANNIAPGGRPPPTLLGTRGNHAASTRLLSMPEKGRKQDRRPVATLLPLIKS | 300 | | | |
| QY | 301 PYIVAYVMVPEKAVAVIGRRATATVMMSPFQAAVNPVETLLNDRKKLETHAPWQI | 360 | | | |
| Db | 301 PYIVAYVMVPEKAVAVIGRRATATVMMSPFQAAVNPVETLLNDRKKLETHAPWQI | 360 | | | |
| QY | 361 GQAVAPREYCYVM | 373 | | | |
| Db | 361 GQAVAPREYCYVM | 373 | | | |
| RESULT 4 | | | | | |
| AAV97747 | | | | | |
| XX | AAV97747 standard: Protein: 473 AA. | | | | |
| XX | AAV97747: | | | | |
| DT | 06-AUG-2001 (first entry) | | | | |
| De | Human Modalsia protein sequence. | | | | |
| XX | | | | | |
| KM | Modalsia: human: G-protein coupled receptor, human[HIV-1; HIV-2; | | | | |
| KM | Polio; cancer; diabetes; obesity; anorexia; bulimia; asthma; hyp; osion; | | | | |
| KM | Parkinson's disease; acute heart failure; hypertension; osteoporosis; | | | | |
| KM | dietary retention; angina pectoris; myocardial infarction; stroke; ulcers; | | | | |
| KM | allergy; benign prostatic hyperplasia; migraine; psyc; the disorder; | | | | |
| KM | neurological disorder; anxiety; schizophrenia; manic depression; | | | | |
| KM | dementia; dementia; severe mental retardation; dyskinesia; therapy; | | | | |
| OS | Modalsia: severe mental retardation; dyskinesia; therapy; | | | | |
| XX | | | | | |
| XX | Human sapiens. | | | | |
| XX | | | | | |
| XX | W0206142844-A2. | | | | |
| XX | 10-MAY-2001. | | | | |
| XX | | | | | |
| XX | 06-Nov-2000: 2000W0-N50541. | | | | |
| XX | | | | | |
| XX | 04-Nov-1999: 9905-040840. | | | | |
| XX | | | | | |
| XX | (SMK) SMTHRLINE: BECHAM C-00P. | | | | |
| XX | (SMK) SMTHRLINE: BECHAM C-00P. | | | | |
| XX | | | | | |
| XX | Zhu Y, Li X, Wang L. | | | | |
| XX | | | | | |
| XX | W01: 2001-3-0827/05. | | | | |

10 N (388): AAAY1486.

11 New Modlist is protein coupled receptor polypeptides and

12 polypeptides, useful for treating certain diseases (e.g., infectious,

13 pain or cancers), in diagnostic assays, or for identifying compounds

14 for therapy.

15 Claim 1: Page 2/2 42pp. Final.

16 This sequence is the human Modlist protein of the invention. The

17 Modlist protein is a member of the G protein coupled receptor family.

18 The Modlist polypeptide and polynucleotide are useful for treating

19 infectious e.g., bacterial, fungal or viral infections particularly those

20 caused by HIV 1 or HIV 2. The Modlist sequences are also useful for

21 treating pain, cancers, diabetes, obesity, anorexia, bulimia, asthma,

22 Parkinson's disease, acute heart failure, hypotension, hypertension,

23 urinary retention, osteoporosis, anion protein, myocardial infarction,

24 stroke, alcohol, allopurinol, benign prostatic hyperplasia, migraine,

25 vomiting, psychodol and neurological disorders (including anxiety,

26 schizophrenia, manic depression, delirium, dementia, and severe mental

27 retardation), dyskinesias, Huntington's disorder, and alcohol delta

28 receptor's syndrome. The Modlist polypeptide and polynucleotide are also

29 useful in diagnostic assays, as well as in identifying compounds

30 (e.g., agonists or antagonists) that are potentially useful in therapy.

31 Sequence 4/4 AA:

Query Match 99.7% Score 1986; 408.22; Length 4/4;
 Identical Similarity 99.7% Identical 100.0%
 Mismatches 4/22 Conservative 0% Mismatches 1; Indels 0; Gaps 0;

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61 and inflammatory hepatohepatitis, ceroid-hepatitis, and inflammation;

62 anti-infective; and tubercle; and influenza; and tuberculosis;

63 and parasitic; and cancer; immune disorders; cardiovascular disorders;

64 neurological disorders; infectious; hepatohepatitis; and therapy; vaccine;

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104 1 JAN 2001; 2001 TWO US01 410.

105 04 FEB 2003; 2000005 0179065.

106 24 FEB 2003; 2000005 0184664.

107 02 MAR 2003; 2000005 0184664.

108 16 MAR 2003; 2000005 0184664.

109 17 MAR 2003; 2000005 0190076.

110 18 MAR 2003; 2000005 0198174.

111 19 MAY 2003; 2000005 0205515.

112 07 JUN 2003; 2000005 0209467.

113 28 JUN 2003; 2000005 0214886.

114 30 JUN 2003; 2000005 0215145.

115 07 JUL 2003; 2000005 0216647.

116 07 JUL 2003; 2000005 0216860.

117 11 JUL 2003; 2000005 0217487.

118 14 JUL 2003; 2000005 0218290.

119 26 JUL 2003; 2000005 0220964.

120 26 JUL 2003; 2000005 0220964.

121 14 AUG 2003; 2000005 0224518.

122 14 AUG 2003; 2000005 0224519.

123 14 AUG 2003; 2000005 0225214.

124 14 AUG 2003; 2000005 0225214.

125 14 AUG 2003; 2000005 0225260.

126 14 AUG 2003; 2000005 0225267.

127 14 AUG 2003; 2000005 0225270.

128 14 AUG 2003; 2000005 0225347.

129 14 AUG 2003; 2000005 0225757.

130 14 AUG 2003; 2000005 0225758.

131 14 AUG 2003; 2000005 0225759.

132 18 AUG 2003; 2000005 0226279.

133 22 AUG 2003; 2000005 0226681.

134 22 AUG 2003; 2000005 0226686.

135 22 AUG 2003; 2000005 0227182.

136 24 AUG 2003; 2000005 0227099.

137 30 AUG 2003; 2000005 0228624.

138 01 SEP 2003; 2000005 0229287.

139 01 SEP 2003; 2000005 0229644.

140 01 SEP 2003; 2000005 0229644.

141 01 SEP 2003; 2000005 0229644.

142 01 SEP 2003; 2000005 0229644.

143 05 SEP 2003; 2000005 0229509.

144 05 SEP 2003; 2000005 0229514.

145 06 SEP 2003; 2000005 0230437.

146 06 SEP 2003; 2000005 0230438.

147 08 SEP 2003; 2000005 0231242.

148 08 SEP 2003; 2000005 0231242.

149 08 SEP 2003; 2000005 0231242.

150 08 SEP 2003; 2000005 0231242.

151 08 SEP 2003; 2000005 0231242.

152 12 SEP 2003; 2000005 0231968.

153 14 SEP 2003; 2000005 0232497.

154 14 SEP 2003; 2000005 0232498.

155 14 SEP 2003; 2000005 0232499.

156 14 SEP 2003; 2000005 0232499.

157 14 SEP 2003; 2000005 0232499.

158 14 SEP 2003; 2000005 0232499.

159 14 SEP 2003; 2000005 0232499.

160 14 SEP 2003; 2000005 0232499.

161 14 SEP 2003; 2000005 0232499.

162 14 SEP 2003; 2000005 0232499.

163 14 SEP 2003; 2000005 0232499.

164 14 SEP 2003; 2000005 0232499.

165 14 SEP 2003; 2000005 0232499.

166 14 SEP 2003; 2000005 0232499.

167 14 SEP 2003; 2000005 0232499.

168 14 SEP 2003; 2000005 0232499.

169 14 SEP 2003; 2000005 0232499.

170 14 SEP 2003; 2000005 0232499.

171 14 SEP 2003; 2000005 0232499.

172 14 SEP 2003; 2000005 0232499.

173 14 SEP 2003; 2000005 0232499.

174 14 SEP 2003; 2000005 0232499.

175 14 SEP 2003; 2000005 0232499.

176 14 SEP 2003; 2000005 0232499.

177 14 SEP 2003; 2000005 0232499.

178 14 SEP 2003; 2000005 0232499.

179 14 SEP 2003; 2000005 0232499.

180 14 SEP 2003; 2000005 0232499.

181 14 SEP 2003; 2000005 0232499.

182 14 SEP 2003; 2000005 0232499.

183 14 SEP 2003; 2000005 0232499.

184 14 SEP 2003; 2000005 0232499.

185 14 SEP 2003; 2000005 0232499.

186 14 SEP 2003; 2000005 0232499.

187 14 SEP 2003; 2000005 0232499.

188 14 SEP 2003; 2000005 0232499.

189 14 SEP 2003; 2000005 0232499.

[illegible]

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| XX | (HUMA) HUMAN CHROME SOL INTC |
| XX | Kosovo CA, Borash St., Kuber SM; |
| XX | WP: 2001-46557-6/50. |
| XX | N PSTR; AA199565. |
| P7 | Isolated digestive system associated polypeptide for treatment, |
| P7 | preventing and/or promoting disorders related to the digestive system |
| P7 | including digestive system cancers and also for testing and detection |
| P7 | e.g. diagnosis - |
| XX | claim 11; SEQ ID NO 77; 509bp + Sequence listed; English. |
| XX | The invention relates to novel genes (AA199548-AA199604) and proteins |
| CC | (AAW99336-AAW99344) useful for preventing, treating or ameliorating |
| CC | certain conditions e.g. by protein or gene therapy. The genes are |
| CC | isolated from a range of human tissues disclosed in the specification. |
| CC | The nucleic acids, proteins, and bodies and (antibodies) are useful |
| CC | in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast |
| CC | and ovarian cancer and other cancers of the internal and, b)ov, bone |
| CC | marrow, breast, gastrointestinal tract, liver, lung or alimentary; |
| CC | (b) immune disorders e.g. Addison's disease, allergies, autoimmune |
| CC | diseases, multiple sclerosis, rheumatoid arthritis and juvenile |
| CC | diabetes; (c) cardiovascular disorders such as myocardial ischaemia; |
| CC | (d) wound healing; (e) neurological disorders e.g. cerebral ataxia and |
| CC | epilepsy; and (f) infectious diseases such as viral, bacterial, fungal |
| CC | and parasitic infections. |
| C2 | Note: The sequence data for this patent did not form part of the |
| C2 | patent specification, but was obtained in electronic format directly |
| C2 | from WHO at ftp://who.int/pub/published_pat_sequences. |
| XX | Sequence 478 AA: |
| SQ | Query Match 99.7% Score 1086; Jm 22; Length 478; |
| SQ | Post Local Similarity 99.7%; Prod. No. 440 217; |
| SQ | Matches 472; Constantive 07; Mismatches 1; Indels 0; Gaps |
| OY | 1 MANTTGEPEEVSNAISPSASAYVKIVLGLDKESLAGNALLSLVIREPAIRKAVYY 60 |
| LB | |
| LB | 6 MNTTGEPEEVSNAISPSASAYVKIYLGLDKESLAGNALLSLVIREPAIRKAVYY 65 |
| OY | 61 LLDLTADLRSAVFEEVLASVRGSSSTLSALSKIVAPMAVLPETHAIRMPTSV 120 |
| LB | |
| LB | 66 LLDLTADLRSAVFEEVLASVRGSSSTLSALSKIVAPMAVLPETHAIRMPTSV 125 |
| OY | 121 RYMALAHNEFYKKRMILMELGAANFMAMLETSMAMPVEPVDTYKFIDEHQWTFEPHHY 180 |
| LB | |
| OY | 126 RYMALAHNEFYKKRMILTCAAFTEBMALTSMAMPVEPVDTYKFIDEHQWTFEPHHY 185 |
| OY | 181 FKANVTACEPMIALVMIAHAHVYSKLAEFEVERHKMKIVGVMPATSNMWIPHPDVAIQ 240 |
| LB | |
| LB | 186 FKANVTACEPMIALVMIAHAHVYSKLAEFEVERHKMKIVGVMPATSNMWIPHPDVAIQ 245 |
| OY | 241 AANAALACRGTGRDPVLLATIKONDIANSRLDMLEEKSGEKGIGEMUYAIIETELWS 300 |
| LB | |
| LB | 246 AANAALACRGTGRDPVLLATIKONDIANSRLDMLEEKSGEKGIGEMUYAIIETELWS 305 |
| OY | 301 DYTVAQVMEVEKAZAVVBRNTALVMMSEAGAAANPVGELNKTKCTTHDAWQSI 360 |
| LB | |
| LB | 306 DYTVAQVMEVEKAZAVVBRNTALVMMSEAGAAANPVGELNKTKCTTHDAWQSI 365 |
| OY | 361 GAAPARPEPYVM 373 |
| LB | |
| LB | 366 GAAPARPEPYVM 378 |

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| | | |
|-----------------------|---|---|
| F1 | Isoamin | 1-37--154 |
| F1 | /Label | Transmembrane_domain |
| F1 | Kozdon | 164...166 |
| F1 | /Label | "Protein kinase C phosphorylation site" |
| F1 | Isoamin | 187...204 |
| F1 | /Label | Transmembrane_domain |
| F1 | Kozdon | 239...244 |
| F1 | /Label | "Protein kinase C phosphorylation site" |
| F1 | Kozdon | 260...265 |
| F1 | /Label | "Protein kinase C phosphorylation site" |
| F1 | Kozdon | 269...271 |
| F1 | /Label | "Protein kinase C phosphorylation site" |
| F1 | Isoamin | 287...308 |
| F1 | /Label | Transmembrane_domain |
| F1 | /Label | 142...144 |
| F1 | /Label | Transmembrane_domain |
| F1 | Kozdon | 144...147 |
| F1 | /Label | "Carboxy terminal intracellular domain" |
| F1 | Kozdon | 371...374 |
| F1 | /Label | "Proteolytic site" |
| XX | W200042774.A1. | |
| XX | 08-JUN-2000. | |
| XX | 24-NOV-1999: | 99WO_05240001. |
| XX | 25-NOV-1999: | 99US_02204822. |
| XX | 24-NOV-1999: | 99US_02204822. |
| XX | (MILL.) MILLERINUM PHARM INC. | |
| XX | Glocksman, MA. Chem M: | |
| XX | MP1: 2E3D-417242/45. | |
| XX | N ESCR: AAA06384. | |
| PT | New polypeptide encoding a G protein coupled receptor for treatment | |
| PT | neuropenia, anemia, thrombocytopenia, congestive heart failure, | |
| PT | myopathy, ischemia, or atherosclerosis - | |
| XX | claim 1: Page 104-105; 112pp; English. | |
| XX | The present sequence is a novel G-protein coupled receptor (GPCR) | |
| XX | designated 1Z216. It has been mapped to the X chromosome, in proximity | |
| XX | to the SH3B-4766 marker. GPCRs are responsible for signal transduction | |
| XX | within a cell. The sequence encoding this protein was identified using an | |
| XX | expressed sequence tag (EST) with homology to GPCR sequences. Proteins | |
| XX | based on the EST sequence were used to identify a cDNA from a prostate | |
| XX | tumorblast cDNA library. Positive clones were sequenced and the | |
| XX | overlapping fragments were assembled to form a cDNA molecule encoding | |
| XX | the present polypeptide. The polypeptide can be used in diagnosis and | |
| XX | treatment GPCR-related disorders such as neuropenia, anemia, | |
| XX | thrombocytopenia, congestive heart failure, myopathy, ischemia, | |
| XX | atherosclerosis, and a wide range of disorders of the brain, skeletal | |
| XX | muscle, colon, CNS, endocrine cells, aorta, kidney, spleen, lung, | |
| XX | liver, and thymus. | |
| SQ | Sequence: 374 AA: | |
| Query Match | 99-00: Score 1474; Pos 21; Length 374; | |
| Host Local Similarity | 99-28: Prod. No. 10215; | |
| Matched | 470; Conservation: 0; Missed clues: 4; Labels: 0; Gap S: | |
| OY | 1 MANTGDPPEPVASALSHSASAVKRVLLGLIMVSLANNALESLIVKEKALKRAAYVF | |
| OB | 1 MANTGGPPPVASALSPSSASAVKRVLLGLIMVSLANNALESLIVKEKALKRAAYVF | |
| OY | 6 LILDLTLAGDKRSAAVTGVVLASVKHSSTLSALSCTVAEMAVLPLFHAKMLPCTCSVL | |
| OB | 5 LILDLTLAGDKRSAAVTGVVLASVKHSSTLSALSCTVAEMAVLPLFHAKMLPCTCSVL | |
| OY | 1 Z1 KYMAIAHHFVAKRMILNIEAATLVAMAILSVAMAPVEHIVLTKKIDELHSGTFPHHY | |

[illegible]

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|-----|-----|-------|-----------------|
| 36 | N-V | 20003 | 200000S-0246603 |
| 37 | N-V | 20003 | 200000S-0246610 |
| 38 | N-V | 20003 | 200000S-0246611 |
| 39 | N-V | 20003 | 200000S-0246613 |
| 40 | N-V | 20003 | 200000S-0246614 |
| 41 | N-V | 20003 | 200000S-0246617 |
| 42 | N-V | 20003 | 200000S-0246618 |
| 43 | N-V | 20003 | 200000S-0246619 |
| 44 | N-V | 20003 | 200000S-0246620 |
| 45 | N-V | 20003 | 200000S-0246621 |
| 46 | N-V | 20003 | 200000S-0246622 |
| 47 | N-V | 20003 | 200000S-0246623 |
| 48 | N-V | 20003 | 200000S-0246624 |
| 49 | N-V | 20003 | 200000S-0246625 |
| 50 | N-V | 20003 | 200000S-0246626 |
| 51 | N-V | 20003 | 200000S-0246627 |
| 52 | N-V | 20003 | 200000S-0246628 |
| 53 | N-V | 20003 | 200000S-0246629 |
| 54 | N-V | 20003 | 200000S-0246630 |
| 55 | N-V | 20003 | 200000S-0246631 |
| 56 | N-V | 20003 | 200000S-0246632 |
| 57 | N-V | 20003 | 200000S-0246633 |
| 58 | N-V | 20003 | 200000S-0246634 |
| 59 | N-V | 20003 | 200000S-0246635 |
| 60 | N-V | 20003 | 200000S-0246636 |
| 61 | N-V | 20003 | 200000S-0246637 |
| 62 | N-V | 20003 | 200000S-0246638 |
| 63 | N-V | 20003 | 200000S-0246639 |
| 64 | N-V | 20003 | 200000S-0246640 |
| 65 | N-V | 20003 | 200000S-0246641 |
| 66 | N-V | 20003 | 200000S-0246642 |
| 67 | N-V | 20003 | 200000S-0246643 |
| 68 | N-V | 20003 | 200000S-0246644 |
| 69 | N-V | 20003 | 200000S-0246645 |
| 70 | N-V | 20003 | 200000S-0246646 |
| 71 | N-V | 20003 | 200000S-0246647 |
| 72 | N-V | 20003 | 200000S-0246648 |
| 73 | N-V | 20003 | 200000S-0246649 |
| 74 | N-V | 20003 | 200000S-0246650 |
| 75 | N-V | 20003 | 200000S-0246651 |
| 76 | N-V | 20003 | 200000S-0246652 |
| 77 | N-V | 20003 | 200000S-0246653 |
| 78 | N-V | 20003 | 200000S-0246654 |
| 79 | N-V | 20003 | 200000S-0246655 |
| 80 | N-V | 20003 | 200000S-0246656 |
| 81 | N-V | 20003 | 200000S-0246657 |
| 82 | N-V | 20003 | 200000S-0246658 |
| 83 | N-V | 20003 | 200000S-0246659 |
| 84 | N-V | 20003 | 200000S-0246660 |
| 85 | N-V | 20003 | 200000S-0246661 |
| 86 | N-V | 20003 | 200000S-0246662 |
| 87 | N-V | 20003 | 200000S-0246663 |
| 88 | N-V | 20003 | 200000S-0246664 |
| 89 | N-V | 20003 | 200000S-0246665 |
| 90 | N-V | 20003 | 200000S-0246666 |
| 91 | N-V | 20003 | 200000S-0246667 |
| 92 | N-V | 20003 | 200000S-0246668 |
| 93 | N-V | 20003 | 200000S-0246669 |
| 94 | N-V | 20003 | 200000S-0246670 |
| 95 | N-V | 20003 | 200000S-0246671 |
| 96 | N-V | 20003 | 200000S-0246672 |
| 97 | N-V | 20003 | 200000S-0246673 |
| 98 | N-V | 20003 | 200000S-0246674 |
| 99 | N-V | 20003 | 200000S-0246675 |
| 100 | N-V | 20003 | 200000S-0246676 |
| 101 | N-V | 20003 | 200000S-0246677 |
| 102 | N-V | 20003 | 200000S-0246678 |
| 103 | N-V | 20003 | 200000S-0246679 |
| 104 | N-V | 20003 | 200000S-0246680 |
| 105 | N-V | 20003 | 200000S-0246681 |
| 106 | N-V | 20003 | 200000S-0246682 |
| 107 | N-V | 20003 | 200000S-0246683 |
| 108 | N-V | 20003 | 200000S-0246684 |
| 109 | N-V | 20003 | 200000S-0246685 |
| 110 | N-V | 20003 | 200000S-0246686 |
| 111 | N-V | 20003 | 200000S-0246687 |
| 112 | N-V | 20003 | 200000S-0246688 |
| 113 | N-V | 20003 | 200000S-0246689 |
| 114 | N-V | 20003 | 200000S-0246690 |
| 115 | N-V | 20003 | 200000S-0246691 |
| 116 | N-V | 20003 | 200000S-0246692 |
| 117 | N-V | 20003 | 200000S-0246693 |
| 118 | N-V | 20003 | 200000S-0246694 |
| 119 | N-V | 20003 | 200000S-0246695 |
| 120 | N-V | 20003 | 200000S-02 |

| | | | | | | | |
|-----------------------|--|--|--------------|------------|---------|--------|---|
| Post Local Similarity | 99.28% | Prot. No. | 4-76-147 | Inserts | 1 | Miss | 0 |
| Matches | 2643 | Conservative | 1 | Mismatches | 1 | Indels | 0 |
| QY | 1 | MANITGEPEVNSALSPESASAVYKIVLGLIMVSLANALISLVLKEPAIKRAYYE | 60 | | | | |
| 1B | 6 | MANITGEPEVNSALSPESASAVYKIVLGLIMVSLANALISLVLKEPAIKRAYYE | 65 | | | | |
| QY | 61 | LIIDPLAAVYKSAVPEPEVIVASVRISSWSPALSLSKIVAIKPAVPEYTHAIRMPEYSL | 120 | | | | |
| 1B | 66 | LIIDPLAAVYKSAVPEPEVIVASVRISSWSPALSLSKIVAIKPAVPEYTHAIRMPEYSL | 125 | | | | |
| QY | 121 | KYMAIAHREYAKRRIIMWTEAAVIGKAMILSSAMAEPEVPEVYKIEHEEQTEPEHY | 180 | | | | |
| 1B | 126 | KYMAIAHREYAKRRIIMWTEAAVIGKAMILSSAMAEPEVPEVYKIEHEEQTEPEHY | 185 | | | | |
| QY | 181 | FRANPLDPEMLMAVIMAAIHAAVSKILLPEYHKKRKIVQVPAISOMIPEHPEYALVQ | 240 | | | | |
| 1B | 186 | FRANPLDPEMLMAVIMAAIHAAVSKILLPEYHKKRKIVQVPAISOMIPEHPEYALVQ | 245 | | | | |
| QY | 241 | AAANGLASPEGRSPMPPTLLATIKONT | 265 | | | | |
| 1B | 246 | AAANGLASPEGRSPMPPTLLATIKONT | 270 | | | | |
| RESULT 10 | | | | | | | |
| 1B | AAV90543 | standard: Protein: 470 AA: | | | | | |
| XX | AAV90543 | | | | | | |
| XX | AAV30543: | | | | | | |
| XX | 15 NOV 1999 | (first entry) | | | | | |
| 1B | A G | protein coupled receptor protein designated SREB2. | | | | | |
| XX | 1B | G protein-coupled receptor protein: SREB2; central nervous system; | | | | | |
| XX | 1B | inflammatory disorder; immunocoupled. | | | | | |
| XX | OS | Homo sapiens: | | | | | |
| XX | 1B | W0946478-A1: | | | | | |
| 1B | 15 SEP 1999. | | | | | | |
| XX | 1B | 11-MAR-1999: 99W01J001191. | | | | | |
| XX | 1B | 12-MAR-1998: 98JP 0060245. | | | | | |
| XX | 1B | 03-FEB-1999: 99JP-0026774. | | | | | |
| XX | 1B | (YAMA) YAMAB053H1 PHABM 70.11D. | | | | | |
| XX | 1B | Matsumoto M, Shimamoto J, Iakasaki J, Saito J, Kunitada M; | | | | | |
| XX | 1B | WPI: 1999-551407/46. | | | | | |
| XX | 1B | N-LSUB; AA210561. | | | | | |
| 1B | G | protein-coupled receptor proteins expressed in the central nervous | | | | | |
| 1B | system and genes encoding them | | | | | | |
| XX | Example 1: Page 53-54; 72pp; Japanese. | | | | | | |
| XX | The present sequence represents a G protein-coupled receptor protein | | | | | | |
| XX | designated SREB2. The protein is expressed in the central nervous | | | | | | |
| XX | system. The SREB2 proteins are used for the diagnosis and treatment | | | | | | |
| XX | of disorders of the central nervous system, including inflammatory | | | | | | |
| XX | disorders of immunocoupled origin. | | | | | | |
| XX | Sequence | 470 AA: | | | | | |
| QY | Post Local Similarity | 64.78% | Score 1298.5 | IR 201 | Locally | 67% | |
| Matches | 245 | Conservative | 56 | Mismatches | 77 | Indels | 7 |
| QY | 1 | MANITGEPEVNSALSPESASAVYKIVLGLIMVSLANALISLVLKEPAIKRAYYE | 60 | | | | |

| | | | | |
|-----|-----|---------------------------------------|-----------------------------------|-----|
| 1b | 1 | MAVNSHADNLTUNISP | LTAFIKLSGAPFGVSVGNLTSLVKRKLHRAVYF | 5b |
| 57 | 61 | LLGLGLALGIRISAVTFFVVLASVGRHSNWPSALSR | GVAFMAVLPFHAAFMLETSVF | 120 |
| 14b | 59 | LLDGVSSTLEPSADTFFVFNVSVRKNSFWYGLTG | FKVLAFLVLSFTEHAFMELSVF | 118 |
| 57 | 121 | GYMAFAHREFAVRKPHETFMVAVIGMAWETLSVMAAF | GVVWVZIKYKTRDEKSGTPEHRY | 180 |
| 14b | 119 | KKLAFAHREFAVRKLTWPLAVIGMAWETLSVMAAF | GVVWVZIKDESGTPEHRY | 178 |
| 57 | 181 | FRANIDLEPLMLVLMVAATFAVYVSKLLFEYRIRKRM | GVGMVAISNNMIFHSAWQ | 241 |
| 14b | 179 | FRANISDLEPLMLALTLATGLVYVTKLFEYHGRKRM | GVFAVSGNMIFHSAWQ | 239 |
| 57 | 241 | AAANALAEFGHGMPLGILGYNHSAAS | KKLAEMGVKDEKLGDMVYALITLITLLW | 299 |
| 14b | 239 | AAANALAEFGHGMPLGILGYNHSAAS | KKLAEMGVKDEKLGDMVYALITLITLLW | 297 |
| 57 | 300 | SVYVAVVWVGVVKA | AVPHRYLATAVVMSFGAANVITVPLINKIKKL | 358 |
| 14b | 299 | SVYVAVVWVGVVKA | AVPHRYLATAVVMSFGAANVITVPLINKIKKL | 357 |
| 57 | 359 | GLGVAVAFREYVGM | SLF | 417 |
| 14b | 358 | KKSLRLKRLVYV | SLF | 416 |

RESULT 11
 AAY0537
 AAY0537 standard; protein; 470 AA.
 AAY0537:
 15 NOV 1999 (first entry)
 A 0 protein coupled receptor protein designated SHERZ.
 0 protein coupled receptor protein; SHERZ; central nervous system;
 inflammatory disorder; immunological.
 05 Rat: 05p
 05 W0934578 AL
 08 16 SEP 1999.
 08 11 MAR 1999; 99WRJ001191.
 08 12 MAR 1998; 98UP0060245.
 08 04 FEB 1999; 99UP0026774.
 (YAMA) YAMAMOTOJI PHARM CO LTD.
 Matsumoto M, Saitohiro T, Takasaki J, Saito T, Kamohara M;
 Waki 1999 55:439/46.
 08 N 19106; MAZ10577.
 08 0 protein coupled receptor proteins expressed in the central nervous
 system and spans encoding them
 Example 4: Page 66 67; Japan.
 The present sequence represents a 0 protein coupled receptor protein,
 designated SHERZ. The protein is expressed in the central nervous
 system. The SHERZ product is used for the diagnosis and treatment
 of diseases of the central nervous system, including inflammatory
 disorders of immunological origin.
 Sequence: 470 AA.
 Entry: Mar 09 64 78. Score: 1286.5; 106.20; Length: 470.

[illegible]

PK 01-OCT-1999; 990S-0176294;
 PK 12-OCT-1999; 990S-0416760;
 PK 12-OCT-1999; 990S-0417044;
 PA (AREN-) ARENA PHARM INC;
 P1 Chen K, Bang HT, Liaw CW, Lin F;
 PK WPT: 2000-40006/64.
 DR N-PSICH; AAA01140;
 PK Novel human orphan G protein-coupled receptors and the encoding cDNAs
 P1 for use in the identification of G protein-coupled receptor agonists -
 XX
 PS Claim 50; Page 74-75; 102pp; English.
 XX
 CC The present amino acid sequence is the hGHR, an endogenous human
 CC orphan G protein-coupled receptor (GPCR), expressed in the foetal brain,
 CC putamen and occipital cortex. The hGHR cDNA was identified using EST
 CC (expressed sequence tag) 46581 as a probe.
 CC The orphan cDNA of the invention, like all GPCRs has seven transmembrane
 CC α -helices with an extracellular N-terminus and an intracellular
 CC C-terminus. However, no endogenous ligands has yet been identified for
 CC the protein of the invention. The orphan GPCRs may be used in the
 CC identification of their endogenous ligands, and to screen potential GPCR
 CC agonists and antagonists for use as pharmaceutical agents. The proteins
 CC may also be used in the study of GPCR-mediated signalling cascades, and
 CC to elucidate their precise role in normal and diseased human conditions.
 CC Nucleic acid encoding human orphan GPCRs may be used for tissue
 CC localisation expression analysis to provide information about their
 CC function in healthy and pathological states.
 XX
 SEQ Sequence 476 AA;
 Query Match 64.7%; Score 1288.5; E0.21; Length 370;
 Best Local Similarity 62.7%; Prod. No. 90148;
 Matches 245; Conservative 56; Mismatches 77; Indels 7; Gaps 4;
 QY 1 MANTICEFEVSGALSPISASAYKVLGLIMVSLANALSLVLRKALHKAAYVE 60
 DE 1 MANSIHADNITLQNLSP 11AFRLPSGLHGVSVGNLISLIVKRIHRAAYVE 58
 XX
 QY 61 LLDPLTADGTSACWCPPEVLASVRHSGSWTPSALSKIVAMAVIECPHAAVECLSVI 120
 DE 59 LLDLCTSLIRKSAICTPPEVSVKNSGWTGTLCKEATLAVLSCHIAMFLKCSVT 118
 XX
 QY 121 KYMALAHREYAKQNTLMTCAAVICMAMLSVAMAFPEVPIVGYKELREHSGTFFEHRY 180
 DE 119 KYLAIAHREYTKRLFWTGLAVICMAMLSVAMAFPEVPIVGYKELREHSGTFFEHRY 178
 XX
 QY 181 PRANITLGFEMLVAMVAHAAVVKLLPEYKIPKKKPVQVQVAVLSNWTFFHRAAGG 240
 DE 179 PRANITLGFEMLVAMVAHAAVVKLLPEYKIPKKKPVQVQVAVLSNWTFFHRAAGG 238
 XX
 QY 241 AAANWIAHCEKQPPHLLTIRKUNHANS-KRLTMDQVKIKGQIGREFAVLLTFLILM 279
 DE 239 AAANWIAHCEKQPPHLLTIRKUNHANS-KRLTMDQVKIKGQIGREFAVLLTFLILM 298
 XX
 QY 400 SPYIVAVYWRVYKACAVTHIKYLAIAVWMSFQAAVNPVPELTKDK; KKK; TTHAKW 358
 DE 299 SPYIVAVYWRVYKACAVTHIKYLAIAVWMSFQAAVNPVPELTKDK; KKK; TTHAKW 357
 XX
 QY 459 GICGAPATKELVYQW 474
 DE 458 -IKSSKIDREYVYI 479
 XX
 PEST: 13
 AA02447
 ID AA02447 standard; Prototag: 470 AA;
 XX
 AA02447
 XX

D1 22-APR-2000 (first entry)
 XX
 DE Human G protein coupled receptor hGHR protein SEQ ID NO:28;
 XX
 KW Human G protein coupled receptor; GPCR; Transmembrane receptor;
 KW identified from agonist screening; therapeutic pharmaceutical;
 KW mutant.
 XX
 OS Homo sapiens.
 XX
 PN W0200022131 A2.
 XX
 ID 20 APR-2000.
 XX
 XX
 PF 14-OCT-1999; 990S-0154605;
 XX
 PK 14-OCT-1999; 990S-0170496;
 PK 12-NOV-1998; 980S-0108029;
 PR 20-NOV-1998; 980S-0109213;
 PR 27-NOV-1998; 980S-0110060;
 PK 16-DEC-1999; 990S-0120416;
 PR 26-DEC-1999; 990S-0121852;
 PR 12-MAR-1999; 990S-0123944;
 PR 12-MAR-1999; 990S-0123945;
 PR 12-MAR-1999; 990S-0123946;
 PR 12-MAR-1999; 990S-0123948;
 PR 12-MAR-1999; 990S-0123949;
 PR 12-MAR-1999; 990S-0123951;
 PR 28-MAY-1999; 990S-0146446;
 PR 28-MAY-1999; 990S-0146447;
 PR 28-MAY-1999; 990S-0146449;
 PR 28-MAY-1999; 990S-0147127;
 PK 28-MAY-1999; 990S-0147131;
 PK 28-MAY-1999; 990S-0147567;
 PK 40-JUN-1999; 990S-0147448;
 PR 27-AUG-1999; 990S-0151114;
 PR 04-SEP-1999; 990S-0152524;
 PR 29-SEP-1999; 990S-0156643;
 PK 29-SEP-1999; 990S-0156655;
 PK 29-SEP-1999; 990S-0156664;
 XX
 PA (AREN-) ARENA PHARM INC;
 XX
 P1 Brian P, Lehmann-Hruska K, Chalmers DL, Chen K, Bang HT;
 P1 Gene M, Liaw CW, Lin F, Liaw C, White G;
 XX
 DR WPT: 2000-417986/27;
 DR N-PSICH; AAA46041;
 XX
 P1 Non-endogenous human G protein coupled receptors for screening
 P1 receptor inverse or partial agonists used as therapeutic agents
 XX
 PS Example 1; Page 104-105; 187pp; English.
 XX
 CC The present invention describes transmembrane receptors, preferably
 CC human G protein coupled receptors (GPCRs), for which the endogenous
 CC ligand is unknown (orphan GPCR receptors). More specifically the present
 CC invention relates to non-endogenous, constitutively activated versions
 CC of a human GPCR. These non-constitutive human GPCRs can be useful for
 CC the direct identification of candidate compounds as receptors agonists -
 CC inverse agonists or partial agonists for use as pharmaceutical agents.
 CC AAA46017 to AAA46126 and AA024825 to AA024859 represent sequences used in
 CC the exemplification of the present invention.
 XX
 SEQ Sequence 470 AA;
 Query Match 64.7%; Score 1288.5; E0.21; Length 370;
 Best Local Similarity 62.7%; Prod. No. 90148;
 Matches 245; Conservative 56; Mismatches 77; Indels 7; Gaps 4;
 QY 1 MANTICEFEVSGALSPISASAYKVLGLIMVSLANALSLVLRKALHKAAYVE 60
 DE 1 MANSIHADNITLQNLSP 11AFRLPSGLHGVSVGNLISLIVKRIHRAAYVE 58
 XX

118 59 GTSISPSLTHGKNNMALLAVLITLITAGNLTAVMANSLEKKUNAI NYITMSLATA 118
 68 68 IRIKSAWCEPEVLAASVROGSSWPSALSCKIVAMAVPEPIHAAVPEPIISVIRYMAIA- 126
 119 DMICAPFVAVSMILLYGKMBLPSKLAZAVYLDVLSIASIMHIAVSLIBEVVALON 178
 127 -HHREYAKRMLIMTCAAVIGMAWTSVAMAP PVHIVYTKYFTRERDQUT-ERKYE 181
 179 EHHSPNSKRAKLIKIAV- WITSVLSMIPVFGQDSKVERKESSTIAONIV 234
 182 KANDIPEMIMAVIMAAVHAAVSKLLEF- -HHKKRPVQVMVAVS- 227
 235 EUGSEVSEPIHLEI MWITVELLTKSLQKALIVSOLITPAKIASPILFUSLSSEKL 293
 228 UNMFRICVA-FOUAAANWIAHGRDMPVILITIPONHAAKRLIGMEYKGRQIG 285
 234 FURSHREKDSYFGRRIMUS- -NECKAKVIG 325
 286 HPEVALITLILMSPIVAVYMWVVK-AC-AVPHRYLAVMMSFAGAAVPIVETL 342
 426 IVPF LIAVWMPPEPIINIMAVIGKESNENIAGALLNVEVWIGYLSAVNPIVYTL 481
 443 INKDLKCLTHAV 457
 482 FNTYKASVRYG 496
 RESULT 8
 US-07 996 772A-11
 Sequence 11, Application US/07996/772A
 Patent No. 5472866
 GENERAL INFORMATION:
 APPLICANT: Gattai, Christopher
 APPLICANT: Bartley, Paul R.
 APPLICANT: Brauchek, Theresa A.
 APPLICANT: Wotushek, Richard A.
 TITLE OF INVENTION: DNA ENCODING 5 HHA SPROUTIN
 TITLE OF INVENTION: RECEPTORS AND USDS THEREOF
 NUMBER OF SEQUENCES: 12
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: COOPER & DENHAM
 STREET: 30 ROCKEFELLER PLAZA
 CITY: NEW YORK
 STATE: NEW YORK
 ZIP: 10112
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: DOS/MS-DOS
 SOFTWARE: Patcut to Release #1.24
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07996/772A
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: White, P., John
 REGISTRATION NUMBER: 28,678
 REFERENCE/WORK NUMBER: 4264/11W/11P
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 977 9650
 TELEFAX: (212) 664-0525
 TELEX: 42523 COOP 01
 INFORMATION FOR SEQ ID NO: 11:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 471 amino acids
 TYPE: amino acid
 STAMENESS: single
 TOPOLOGY: linear
 MEDIUM TYPE: PROTO
 IMMEDIATE SOURCE:
 COUNTRY: 5 HT2
 US-07-996-772A 11

Query Match 13.08; Score 259.5; DB 1; Length 471;
 Best Local Similarity 24.48; P-Val 1.4e-15;
 Matches 90; Conserved 68; Mismatches 150; Indels 61; Gaps 14;
 17 PPSAAVVKI-----VILIMVSLAGNALSLVKEKAIKRAVYELITCAVAG 99
 62 PPTSLTHGKNNMALLIVITLITAGNLTAVMANSLEKKUNAI NYITMSLATA 121
 70 IBSAVPEVLAASVROGSSWPSALSCKIVAMAVPEPIHAAVPEPIISVIRYMAIA 126
 122 EUGSEVSEPIHLEI MWITVELLTKSLQKALIVSOLITPAKIASPILFUSLSSEKL 161
 127 -HHREYAKRMLIMTCAAVIGMAWTSVAMAP PVHIVYTKYFTRERDQUT-ERKYE 184
 182 HIRPNSKRAKLIKIAV- WITSVLSMIPVFGQDSKVERKESSTIAONIV 237
 184 NDITGEMIMAVIMAAVHAAVSKLLEF- -HHKKRPVQVMVAVS-ALSNMITH 233
 238 GSVAPPEPIHLEI MWITVELLTKSLQKALIVSOLITPAKIASPILFUSLSSEKL 275
 234 GPCATGAAANWIAHGRDMPVILITIPONHAAKRLIG MEYKGRQIGRPIV 291
 296 -----GRSH -----REDSYAKRIMDSINCKAKVITVEF 300
 292 LILFLMSPIVAVYMWVVK AC-AVPHRYLAVMMSFAGAAVPIVETL 348
 431 LEVWMPPEPIINIMAVIGKESNENIAGALLNVEVWIGYLSAVNPIVYTL 488
 449 KCLTHAV 457
 489 SAVRYG 497
 RESULT 9
 US-09 632 742-Z
 Sequence 2, Application US/09632/742
 Patent No. 6255389
 GENERAL INFORMATION:
 APPLICANT: Bellor, M11
 APPLICANT: Hotick, David, Kathleen
 APPLICANT: Egan, Christina C.
 TITLE OF INVENTION: Constitutively Activated Sproutins
 TITLE OF INVENTION: Receptors
 NUMBER OF SEQUENCES: 25
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Laurence Weinberger
 STREET: 882 S. Market Street, Suite 103
 STREET: P.O. Box 1663
 CITY: West Chester
 STATE: PA
 COUNTRY: USA
 ZIP: 19380 0054
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patcut to Release #1.0, Version #1.10
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09632/742
 FILING DATE: 27 FEB 1998
 CLASSIFICATION: 536
 ATTORNEY/AGENT INFORMATION:
 NAME: Weinberger, Laurence
 REGISTRATION NUMBER: 27,965
 REFERENCE/WORK NUMBER: 3084-4
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (610) 431-1708
 TELEFAX: (610) 431-1141
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 471 amino acids
 TYPE: amino acid

1 ORGANISM: HUMAN
2 Database: not relevant
3 Molecule type: protein
4 US 09 042 742 2

Query Match 14.0% Score 259.52 Id 42 Length 471

Best local similarity 24.4% Prod. No. 1.4e 152
Method: 902 Conserved 982 Mismatches 1502 Indels 612 Gaps 142

17 PPSASAVYK: VLLGLIMVSLAGNALLSLVLEKRAHKAAYEELIAGTLAG 69

18 62 PPTGTSLLHGRKNSALLTIVVLTITANNTIVMAVSEKRLQNAINTFRLSTALIM 121

19 70 IRSAVPEPVAVSRHSMTFSALSRKIVAFMAVLPCHAAFMPLSVIRYMAIA 126

20 122 LQELVAVSRKILLEVYRPLSKIVAVIYVLFSTIMHICVMSIDQVVALVGN 181

21 127 HIRYAKRRLTWVAAVGMWLTSSVMAATPVPVAVGYKRLKEEDGTFPIRYEKA 183

22 182 HIRSNRKRKAKRTIAV WTSVGLSMDIPVAVLQSKVKRSTTADNVEVL 247

23 184 NDLRRLMIAVIMAHVYKELIFE YIRKRKPVMVAP AISNWIPEH 243

24 248 GSVAVPFTLITVITVPLTSLQKFAVLSVSLSTAKLSTSLQSSSKRLE 295

25 254 GYVATVGAANMIAEGGEGMPPTTLTKGNHAASTRLLT MEVYKRLAKRPMVAT 291

26 296 GRSIH RRRSVYAKRIMQSTSNQKAKVATVVF 340

27 292 TLFTLLMSYIVAVYKRVK AC AVIRKRLATAVMSSTVGAANVIVTLNKLK 348

28 341 LFWVMVPEFTINIAVIGKSNENVIQALLNVEVWIGYLSAVNIVLTAKRYK 388

29 349 KTLTHAT 357

30 389 SAKSTGT 397

RESULT 11
US 09 145 864 4

1 Sequence 4: Application US/09145864

2 Patent No. 6487562

3 GENERAL INFORMATION:

4 APPLICANT: Kary, Hugo Tech

5 APPLICANT: Hugo Tech, Paul R.

6 APPLICANT: Biotechnology, Biotech

7 TITLE OF INVENTION: DNA Encoding A Human Secretorin (s) H12 Receptor and

8 TITLE OF INVENTION: Uses thereof

9 FILING REFERENCE: 4599/0467/HW

10 CURRENT APPLICATION NUMBER: US/09/145,864

11 CURRENT FILING DATE: 1999 09 02

12 NUMBER OF SEQ ID NOS: 4

13 SEQUENCE: Patent to Vol. 2.1

14 SEQ ID NO: 4

15 LENGTH: 471

16 TYPE: PRT

17 ORGANISM: Hominid non primate

18 US 09 145 864 4

Query Match 14.0% Score 259.52 Id 42 Length 471

Best local similarity 24.4% Prod. No. 1.4e 152

Method: 902 Conserved 982 Mismatches 1502 Indels 612 Gaps 142

17 PPSASAVYK: VLLGLIMVSLAGNALLSLVLEKRAHKAAYEELIAGTLAG 69

18 62 PPTGTSLLHGRKNSALLTIVVLTITANNTIVMAVSEKRLQNAINTFRLSTALIM 121

19 70 IRSAVPEPVAVSRHSMTFSALSRKIVAFMAVLPCHAAFMPLSVIRYMAIA 126

20 122 LQELVAVSRKILLEVYRPLSKIVAVIYVLFSTIMHICVMSIDQVVALVGN 181

21 127 HIRYAKRRLTWVAAVGMWLTSSVMAATPVPVAVGYKRLKEEDGTFPIRYEKA 183

22 182 HIRSNRKRKAKRTIAV WTSVGLSMDIPVAVLQSKVKRSTTADNVEVL 247

23 184 NDLRRLMIAVIMAHVYKELIFE YIRKRKPVMVAP AISNWIPEH 243

184 HIRSNRKRKAKRTIAV WTSVGLSMDIPVAVLQSKVKRSTTADNVEVL 247

184 NDLRRLMIAVIMAHVYKELIFE YIRKRKPVMVAP AISNWIPEH 243

248 GSVAVPFTLITVITVPLTSLQKFAVLSVSLSTAKLSTSLQSSSKRLE 295

254 GYVATVGAANMIAEGGEGMPPTTLTKGNHAASTRLLT MEVYKRLAKRPMVAT 291

296 GRSIH RRRSVYAKRIMQSTSNQKAKVATVVF 340

292 TLFTLLMSYIVAVYKRVK AC AVIRKRLATAVMSSTVGAANVIVTLNKLK 348

341 LFWVMVPEFTINIAVIGKSNENVIQALLNVEVWIGYLSAVNIVLTAKRYK 388

349 KTLTHAT 357

389 SAKSTGT 397

RESULT 11
US 09 292 071 44

1 Sequence 33: Application US/09292071

2 Patent No. 6107424

3 GENERAL INFORMATION:

4 APPLICANT: Indian, Pontific

5 APPLICANT: Galileos, Fortick

6 TITLE OF INVENTION: No. 6107424 Endogenous, Constitutively Activated

7 TITLE OF INVENTION: Human Secretorin Receptors and Small Molecule Modulators The

8 NUMBER OF SEQUENCES: 44

9 CORRESPONDING ADDRESS:

10 ADDRESS: Alameda Pharmaceutical, Inc.

11 STREET: 6146 N. Main Rd. Suite 100

12 CITY: San Diego

13 STATE: CA

14 COUNTRY: USA

15 ZIP: 92121

16 COMPUTER READABLE FORM:

17 MEDIUM TYPE: floppy disk

18 OPERATING SYSTEM: IBM PC compatible

19 SOFTWARE: Patent to Receptor #1.0, Version #1.0

20 CURRENT APPLICATION DATA:

21 APPLICATION NUMBER: US/09/292,071

22 FILING DATE: April 14, 1999

23 CLASSIFICATION:

24 NAME: Mark J. Rosen

25 REGISTRATION NUMBER: 49,862

26 TELEPHONE: (215) 564-6525

27 TELEPHONE: (215) 568-4409

28 INFORMATION FOR SEQ ID NO: 44

29 SEQUENCE CHARACTERISTICS:

30 LENGTH: 478 amino acids

31 TYPE: amino acid

32 STRANDEDNESS:

33 Topology: not relevant

34 Molecule type: protein

US 09 292 071 44

Query Match 14.0% Score 259.52 Id 42 Length 478

Best local similarity 24.4% Prod. No. 1.4e 152

Method: 972 Conserved 722 Mismatches 1612 Indels 522 Gaps 142

17 PPSASAVYK: VLLGLIMVSLAGNALLSLVLEKRAHKAAYEELIAGTLAG 69

18 62 PPTGTSLLHGRKNSALLTIVVLTITANNTIVMAVSEKRLQNAINTFRLSTALIM 119

19 67 ALAIRSAVPEPVAVSRHSMTFSALSRKIVAFMAVLPCHAAFMPLSVIRYMAIA 126

20 112 LQELVAVSRKILLEVYRPLSKIVAVIYVLFSTIMHICVMSIDQVVALVGN 178

21 119 ALIRYAKRRLTWVAAVGMWLTSSVMAATPVPVAVGYKRLKEEDGTFPIRYEKA 180

DB 694 1YKAPSNIYLR 405

RESULT 14

US 09 292 071 41

Sequence 41, Application US/09/292071

Patent No. 6107424

GENERAL INFORMATION:

APPLICANT: Rohan, Dominik

APPLICANT: Chalmers, Derek J

TITLE OF INVENTION: No. 6107424 Endogenous, Constitutively Activated Human

TITLE OF INVENTION: Human Secretin Receptors and Small Molecule Modulators Thereof

NUMBER OF SEQUENCES: 4

ADDRESS/SEQUENCE ADDRESS:

ADDRESS: Actigra Pharmaceuticals, Inc.

STREET: 6166 Nancy Ridge Drive

CITY: San Diego

STATE: CA

COUNTRY: USA

DATE: 9/21/01

COMPUTER REMARKS FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/292071

FILING DATE: April 14, 1999

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Mark J. Rosen

REGISTRATION NUMBER: 69,842

FEDERAL REGISTRATION INFORMATION:

TELEPHONE: (215) 564 5525

TELEFAX: (215) 564 5439

INFORMATION FOR SEQ ID NO: 41:

SEQUENCE CHARACTERISTICS:

LENGTH: 478 amino acids

TYPE: amino acid

STANDARDNESS:

COMPLEXITY: not relevant

MODIFIABLE TYPE: protein

US 09 292 071 41

Query Match 14.0% Score 298; DB 4; Length 478;

Best Local Similarity 24.1% Prod. No. 1,96-15;

Matches 85; Conserved 72; Mismatches 167; Indels 44; Gaps 12;

DB 14 GALSPPASAV VKVLVLLIMCVSLANRALLSLVLEKPKALIKAPYFLLDGL 66

DB 59 GTLSSTSLIHGGRKMSALLAVVLTITLVNLTIVMANSLEKKLCNATNPTKSLAI 118

DB 67 AALTRSAVPEPVLAASVGRSSMTSPALSRTIVAFMAVLPVTHAAMPQTSVRYMAIA 126

DB 119 AMLALGELVMSRLILLYGYMPLPSKLVAVLYLVLPSTASIMLVASIDRVVALY 178

DB 127 IHREYAKRKETLWTAAVFMAVLSVAMAPFVPTVQVLYKRLREEDAPTE EHRV 180

DB 179 NPTHRSKRSKAKPLKLVAVWLSVLSMPLVYVGLQDSKVKRKSSTLADQNF 244

DB 181 FRANPLLEPMIMAVIMAAVIAVYKLTLLPEYRRKKKKV VQNVATISQNWTF 242

DB 245 VLTGSVSEFTPLT MVLTFTPLTKVLRQALMLDHLHFEEDLSEDLKVKRN 290

DB 244 HPGVATLQAAANNAVGRGPMPTLLTGQNHAASTRLLIMHEVKRGQLRKKYATF 292

DB 291 TAEHNSAN PNDGNARRKKRRKRPRGIMQAINNRKRSKVAIVF 347

DB 293 LLETLMSVIVAYWGVYKAV AVIRKYLATAVMSFPAVAVNPVTVLLNKIKR 449

DB 448 ELVVVWMPPEFTINIMAVTKRSNIEAVTCALLNVVTVGYLSAVNPVTVLLPKIKYR 497

DB 450 VLLIHAT 457

DB 694 AFSNYLR 405

RESULT 15

US 09 292 069A 41

Sequence 41, Application US/09/292069A

Patent No. 6140509

GENERAL INFORMATION:

APPLICANT: Rohan, Dominik

APPLICANT: Chalmers, Derek J

TITLE OF INVENTION: No. 6140509 Endogenous, Constitutively Activated Human

TITLE OF INVENTION: Secretin Receptors And Small Molecule Modulators

NUMBER OF SEQUENCES: 4

ADDRESS/SEQUENCE ADDRESS:

ADDRESS: Actigra Pharmaceuticals, Inc.

STREET: 6166 Nancy Ridge Drive

CITY: San Diego

STATE: CA

COUNTRY: USA

DATE: 9/21/01

COMPUTER REMARKS FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/292069A

FILING DATE: April 14, 1999

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Mark J. Rosen

REGISTRATION NUMBER: 69,842

FEDERAL REGISTRATION INFORMATION:

TELEPHONE: (215) 564 5525

TELEFAX: (215) 564 5439

INFORMATION FOR SEQ ID NO: 41:

SEQUENCE CHARACTERISTICS:

LENGTH: 478

TYPE: amino acid

STANDARDNESS:

COMPLEXITY: not relevant

MODIFIABLE TYPE: protein

US 09 292 069A 41

Query Match 14.0% Score 298; DB 4; Length 478;

Best Local Similarity 24.1% Prod. No. 1,96-15;

Matches 85; Conserved 72; Mismatches 167; Indels 44; Gaps 12;

DB 14 GALSPPASAV VKVLVLLIMCVSLANRALLSLVLEKPKALIKAPYFLLDGL 66

DB 59 GTLSSTSLIHGGRKMSALLAVVLTITLVNLTIVMANSLEKKLCNATNPTKSLAI 118

DB 67 AALTRSAVPEPVLAASVGRSSMTSPALSRTIVAFMAVLPVTHAAMPQTSVRYMAIA 126

DB 119 AMLALGELVMSRLILLYGYMPLPSKLVAVLYLVLPSTASIMLVASIDRVVALY 178

DB 127 IHREYAKRKETLWTAAVFMAVLSVAMAPFVPTVQVLYKRLREEDAPTE EHRV 180

DB 179 NPTHRSKRSKAKPLKLVAVWLSVLSMPLVYVGLQDSKVKRKSSTLADQNF 244

DB 181 FRANPLLEPMIMAVIMAAVIAVYKLTLLPEYRRKKKKV VQNVATISQNWTF 242

DB 245 VLTGSVSEFTPLT MVLTFTPLTKVLRQALMLDHLHFEEDLSEDLKVKRN 290

DB 244 HPGVATLQAAANNAVGRGPMPTLLTGQNHAASTRLLIMHEVKRGQLRKKYATF 292

DB 291 TAEHNSAN PNDGNARRKKRRKRPRGIMQAINNRKRSKVAIVF 347

DB 293 LLETLMSVIVAYWGVYKAV AVIRKYLATAVMSFPAVAVNPVTVLLNKIKR 449

DB 448 ELVVVWMPPEFTINIMAVTKRSNIEAVTCALLNVVTVGYLSAVNPVTVLLPKIKYR 497

DB 450 VLLIHAT 457

DB 498 AFSNYLR 405

Mon Feb '3 11:23:16 2003

us-09-875-076-20.ra1

Page 9

Search completed: February 2, 2003, 08:01:49
Index time: 22 secs

Sequence version 5.1.4
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Method: fastcd, search, used sw model

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(with boot alignment) 402.741 million calls updated/sec

Hit list: US-09-875-076-20
Footprint score: 1902
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Search labels: EUS00862
Gapop 10.0, Gapext 0.5

Searches: 122226 seqs, 20178551 residues

Total number of hits satisfying chosen parameters: 122226

Minimum hit seq length: 0
Maximum hit seq length: 200000000

Post processing: Minimum Match 38
Maximum Match 100%

Listing first 45 summaries

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Published Applications: MA*
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11: /cgn2_6/p/codata/1/pubpa/US09_NEM_P00_P00*
12: /cgn2_6/p/codata/1/pubpa/US09_NEM_P00_P00*
13: /cgn2_6/p/codata/1/pubpa/US09_NEM_P00_P00*
14: /cgn2_6/p/codata/1/pubpa/US09_NEM_P00_P00*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Match | Length DB | ID | Database |
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| 1 | 1977 | 99.2 | 373 | 10 | US-09-760-454A-2 |
| 2 | 1288.5 | 64.7 | 373 | 9 | US-10-04-945-2 |
| 3 | 920 | 46.2 | 184 | 9 | US-09-989-442-111 |
| 4 | 920 | 46.2 | 184 | 10 | US-09-764-894-592 |
| 5 | 734 | 46.8 | 180 | 10 | US-09-989-442-107 |
| 6 | 734 | 46.8 | 180 | 10 | US-09-764-854-567 |
| 7 | 408 | 20.5 | 100 | 10 | US-09-760-454A-4 |
| 8 | 439 | 17.0 | 144 | 9 | US-09-989-442-112 |
| 9 | 439 | 17.0 | 144 | 10 | US-09-764-854-560 |
| 10 | 259.5 | 14.0 | 471 | 10 | US-09-929-413-4 |
| 11 | 257 | 12.9 | 470 | 9 | US-10-166-101-8 |
| 12 | 257 | 12.9 | 471 | 8 | US-08-681-219-30 |
| 13 | 257 | 12.9 | 471 | 10 | US-09-929-413-2 |
| 14 | 244.5 | 12.2 | 471 | 10 | US-09-989-861-17 |
| 15 | 236 | 11.8 | 481 | 8 | US-08-681-219-41 |
| 16 | 236 | 11.8 | 481 | 10 | US-09-919-497-72 |
| 17 | 232 | 11.8 | 445 | 10 | US-09-989-861-16 |
| 18 | 232 | 11.6 | 460 | 9 | US-10-166-101-4 |
| 19 | 231.5 | 11.6 | 451 | 10 | US-09-994-844-6 |

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| 26 | 221.5 | 11.1 | 426 | 10 | US-09-828-548-24 |
| 27 | 221.5 | 11.1 | 426 | 10 | US-09-961-848-2 |
| 28 | 220.5 | 11.1 | 460 | 10 | US-09-951-622-11 |
| 29 | 219 | 11.0 | 460 | 10 | US-09-989-861-18 |
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| 31 | 217 | 10.9 | 445 | 9 | US-09-166-444-5 |
| 32 | 217 | 10.9 | 445 | 10 | US-09-850-206-5 |
| 33 | 215 | 10.8 | 470 | 9 | US-10-109-5428-2 |
| 34 | 215 | 10.8 | 447 | 9 | US-10-077-876-2 |
| 35 | 215 | 10.8 | 447 | 10 | US-09-825-924-2 |
| 36 | 214.5 | 10.8 | 376 | 9 | US-10-166-101-5 |
| 37 | 214.5 | 10.8 | 445 | 9 | US-09-409-755-2 |
| 38 | 214.5 | 10.8 | 445 | 9 | US-09-166-444-2 |
| 39 | 214.5 | 10.8 | 445 | 10 | US-09-450-206-2 |
| 40 | 214 | 10.7 | 377 | 12 | US-10-005-010-2 |
| 41 | 213.5 | 10.7 | 359 | 10 | US-09-989-861-19 |
| 42 | 213.5 | 10.7 | 450 | 9 | US-10-077-870-4 |
| 43 | 213.5 | 10.7 | 450 | 10 | US-09-825-924-4 |
| 44 | 213 | 10.7 | 497 | 12 | US-10-052-589-2 |
| 45 | 213 | 10.7 | 517 | 10 | US-09-951-622-10 |

ALIGNMENTS

RESULT 1

US-09-760-454A-2
Sequence 2, Appl 1
Footprint No. US-09-760-454A-2

GENERAL INFORMATION:

APPLICANT: Bioscience, Inc.

APPLICANT: Bioscience, Inc.

TITLE OF INVENTION: CLONING OF A NOVEL 71M PROTEIN FOR AXON-2

FILE REFERENCE: G070443-21

CURRENT APPLICATION NUMBER: US-09-760-454A

CURRENT FILING DATE: 2001-01-12

PRIOR APPLICATION NUMBER: US-09-008-034

PRIOR FILING DATE: 1998-04-24

PRIOR APPLICATION NUMBER: US-09-277-408

PRIOR FILING DATE: 1999-03-25

NUMBER OF SEQ ID NOS: 4

SOFTWARE: FASTED for Windows Version 4.0

SEQ ID NO 2

LENGTH: 474

TYPE: PRT

ORGANISM: HOMO SAPIENS

US-09-760-454A-2

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| Best Local Similarity | 99.2% | Prod. No. 2, 46-182 | | |
| Matches | 370 | Conservative | 0 | Mismatches 4 |

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| US-09-760-454A-2 | 1 | MANTTREFEVSALSTPSA.....HAWWITGATATRETCVM 474 | Sequence 2, Appl 1 |
| US-09-760-454A-2 | 2 | US-10-04-945-2 | Sequence 2, Appl 1 |
| US-09-760-454A-2 | 3 | US-09-989-442-111 | Sequence 2, Appl 1 |
| US-09-760-454A-2 | 4 | US-09-764-894-592 | Sequence 2, Appl 1 |
| US-09-760-454A-2 | 5 | US-09-989-442-107 | Sequence 2, Appl 1 |
| US-09-760-454A-2 | 6 | US-09-764-854-567 | Sequence 2, Appl 1 |
| US-09-760-454A-2 | 7 | US-09-760-454A-4 | Sequence 2, Appl 1 |
| US-09-760-454A-2 | 8 | US-09-989-442-112 | Sequence 2, Appl 1 |
| US-09-760-454A-2 | 9 | US-09-764-854-560 | Sequence 2, Appl 1 |
| US-09-760-454A-2 | 10 | US-09-929-413-4 | Sequence 2, Appl 1 |
| US-09-760-454A-2 | 11 | US-10-166-101-8 | Sequence 2, Appl 1 |
| US-09-760-454A-2 | 12 | US-08-681-219-30 | Sequence 2, Appl 1 |
| US-09-760-454A-2 | 13 | US-09-929-413-2 | Sequence 2, Appl 1 |
| US-09-760-454A-2 | 14 | US-09-989-861-17 | Sequence 2, Appl 1 |
| US-09-760-454A-2 | 15 | US-08-681-219-41 | Sequence 2, Appl 1 |
| US-09-760-454A-2 | 16 | US-09-919-497-72 | Sequence 2, Appl 1 |
| US-09-760-454A-2 | 17 | US-09-989-861-16 | Sequence 2, Appl 1 |
| US-09-760-454A-2 | 18 | US-10-166-101-4 | Sequence 2, Appl 1 |
| US-09-760-454A-2 | 19 | US-09-994-844-6 | Sequence 2, Appl 1 |

[illegible]

1 DS 10 043 945, 2
 2 Sequence: 2, Application: DS/1004 945
 3 Identification No.: DS20021198 60A1
 4 GENERAL INFORMATION:
 5 APPLICANT: Smith, Kelli E.
 6 APPLICANT: Pathirana, Mattie Sudum
 7 APPLICANT: Kyaw, Hla
 8 APPLICANT: Kozlovsky, Iosh E.
 9 TITLE OF INVENTION: DNA ENCODING COGNON SNOPES, REPEATOR
 10 FILE REFERENCE: 58001
 11 CURRENT APPLICATION NUMBER: DS/10/043, 945
 12 PRIORITY APPLICATION NUMBER: 2002 01 10
 13 PRIORITY APPLICATION NUMBER: 09/264, 041
 14 NUMBER OF SEQ. ID NOS: 2
 15 SEQ. NO. 1: SEQ. NO. 2
 16 SEQ. NO. 2
 17 LENGTH: 670
 18 TYPE: CDS
 19 ORGANISM: Homo sapiens
 20 DS 10 043 945, 2

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| Country Match | 64, 78; | Scored 1288-9; | Dfr 9; | Length 470; |
| Best local similarity | 62, 78; | Prod. No. 4, 20-16; | | |
| Matchos | 245; | Conservation | 77; | Indols 7; |
| | | Matchos | 77; | Caps 4 |

[illegible][illegible]

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| 2 | Sequence 111: Application US/09/089442 |
| 3 | Publication No.: US2010/001664A1 |
| 4 | CLAIMS: INFORMATION |
| 5 | APPENDIX: BOSTON, et al. |
| 6 | 1. LITTLE OF INVENTION: Non-Infectious, Protective, and Anticancer |
| 7 | 2. LITTLE REFERENCE: P1008 |
| 8 | 3. CURRENT APPLICATION NUMBER: US/09/089,442 |
| 9 | 4. CURRENT FILING DATE: 2001-11-21 |
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Matches 1765 Conservative 11 Mismatches 11 Indels 0 Gaps 0

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RESULT 4

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11 PREFIX APPLICATION NUMBER: 60/241,846
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14 PREFIX FILING DATE: 2000-10-20
15 PREFIX APPLICATION NUMBER: 60/241,221
16 PREFIX FILING DATE: 2000-10-20
17 PREFIX APPLICATION NUMBER: 60/246,475
18 PREFIX FILING DATE: 2000-11-09
19 PREFIX APPLICATION NUMBER: 60/241,244
20 PREFIX FILING DATE: 2000-09-08
21 PREFIX APPLICATION NUMBER: 60/244,065
22 PREFIX FILING DATE: 2000-09-14
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US 09 / 64 054 56.7

Query Match 60.88% Score 744 108 102 10000 1000

Best Local Similarity 96.68% Ident. No. 2,46 643

Mismatches 144 Conserved size 07 Mismatches 41 Indels 27 Gaps 12

US 1 MANTGEEVSAVSSASAVYKVLGLIMVSIADNAAHSLMKEKALAKAYVF 60

1b 6 MANTGEEVSAVSSASAVYKVLGLIMVSIADNAAHSLMKEKALAKAYVF 65

US 64 ELIOLTAIRSVGEEVYASVHSSKIFSAISRIVAMAVIPQIAKMLPETSF 120

1b 66 ELIOLTAIRSVGEEVYASVHSSKIFSAISRIVAMAVIPQIAKMLPETSF 125

US 121 PYMAIAHREYAKQDTLWTAAVTCMAV 148

1b 126 PYMAIAHREYAKQDTLWTAAVTCMAV 151

RESULT 7

US 09 / 64 054A 4

Sequence 4: Application US/09760-04A

Patent No. US2002004248A1

GENERAL INFORMATION:

APPLICANT: Ingersoll, Jack S.

APPLICANT: Fishbaugh, Nathan

TITLE OF INVENTION: COMBINATION OF A NOVEL TIM RECEPTOR AND/OR 2

FILE REFERENCE: JP 2004-01

CURRENT APPLICATION NUMBER: US/09/760, 04A

PRIOR APPLICATION NUMBER: US 60/083, 034

PRIOR FILING DATE: 1998 04 24

PRIOR APPLICATION NUMBER: US 09/277, 938

PRIOR FILING DATE: 1999-03-25

NUMBER OF SEQ. ID NOS: 4

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 4

LENGTH: 100

TYPE: PRT

ORGANISM: Homo sapiens

FEATURES:

NAME/KEY: UNCLONE

LOCATION: (9) (80)

OTHER INFORMATION: OTHER INFORMATION: Peptide Sequences Encoded by EST Sequence

US 09 / 64 054A 4

Query Match 20.56% Score 408 108 102 1000

Best Local Similarity 80.08% Ident. No. 2,46 643

Mismatches 107 Conserved size 07 Mismatches 172 Indels 02 Gaps 02

US 177 EHKERANDLDEPMIAVIMAVIYVYKLLFEYRKRKKVQNYVAISQMTPEIG 246

1b 1 EHKERANDLDEPMIAVIMAVIYVYKLLFEYRKRKKVQNYVAISQMTPEIG 250

US 237 ATGGAANWIAAGGGRDHPPTLDTGNDHANSKRLAKMD 276

1b 61 ATGGAANWIAAGGGRDHPPTLDTGNDHANSKRLAKMD 100

RESULT 8

US 09 / 64 054 112

Sequence 112: Application US/20000442

Patent No. US2001001669A1

GENERAL INFORMATION:

APPLICANT: Ingersoll, Jack S.

APPLICANT: Fishbaugh, Nathan

TITLE OF INVENTION: Nucleotide Acids, Proteins, and Antibodies

FILE REFERENCE: P1208

CURRENT APPLICATION NUMBER: US/09/760, 442

PRIOR FILING DATE: 2001 11 21

PRIOR APPLICATION NUMBER: 60/179, 065

PRIOR FILING DATE: 2000 01 31

PRIOR APPLICATION NUMBER: 60/180, 628

PRIOR FILING DATE: 2000 02 04

PRIOR APPLICATION NUMBER: 60/214, 886

PRIOR FILING DATE: 2000 04 28

PRIOR APPLICATION NUMBER: 60/217, 487

PRIOR FILING DATE: 2000 07 11

PRIOR APPLICATION NUMBER: 60/225, 758

PRIOR FILING DATE: 2000 08 14

PRIOR APPLICATION NUMBER: 60/220, 964

PRIOR FILING DATE: 2000 07 26

PRIOR APPLICATION NUMBER: 60/217, 496

PRIOR FILING DATE: 2000 07 11

PRIOR APPLICATION NUMBER: 60/225, 447

PRIOR FILING DATE: 2000 08 14

PRIOR APPLICATION NUMBER: 60/218, 290

PRIOR FILING DATE: 2000 07 14

PRIOR APPLICATION NUMBER: 60/225, 757

PRIOR FILING DATE: 2000 08 14

PRIOR APPLICATION NUMBER: 60/226, 868

PRIOR FILING DATE: 2000 08 22

PRIOR APPLICATION NUMBER: 60/216, 647

PRIOR FILING DATE: 2000 07 07

PRIOR APPLICATION NUMBER: 60/225, 270

PRIOR FILING DATE: 2000 08 14

PRIOR APPLICATION NUMBER: 60/251, 869

PRIOR FILING DATE: 2000 12 08

PRIOR APPLICATION NUMBER: 60/249, 864

PRIOR FILING DATE: 2000 09 27

PRIOR APPLICATION NUMBER: 60/244, 274

PRIOR FILING DATE: 2000 09 21

PRIOR APPLICATION NUMBER: 60/244, 224

PRIOR FILING DATE: 2000 09 21

PRIOR APPLICATION NUMBER: 60/228, 924

PRIOR FILING DATE: 2000 08 30

PRIOR APPLICATION NUMBER: 60/224, 518

PRIOR FILING DATE: 2000 08 14

PRIOR APPLICATION NUMBER: 60/246, 469

PRIOR FILING DATE: 2000 09 29

PRIOR APPLICATION NUMBER: 60/224, 519

PRIOR FILING DATE: 2000 08 14

PRIOR APPLICATION NUMBER: 60/220, 964

PRIOR FILING DATE: 2000 07 26

PRIOR APPLICATION NUMBER: 60/241, 785

PRIOR FILING DATE: 2000 10 20

PRIOR APPLICATION NUMBER: 60/244, 617

PRIOR FILING DATE: 2000 11 01

PRIOR APPLICATION NUMBER: 60/225, 268

PRIOR FILING DATE: 2000 08 14

PRIOR APPLICATION NUMBER: 60/246, 468

PRIOR FILING DATE: 2000 09 29

PRIOR APPLICATION NUMBER: 60/251, 866

PRIOR FILING DATE: 2000 12 08

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PRIOR FILING DATE: 2000 12 08

PRIOR APPLICATION NUMBER: 60/229, 444

PRIOR FILING DATE: 2000 09 01

PRIOR APPLICATION NUMBER: 60/244, 997

PRIOR FILING DATE: 2000 09 25

PRIOR APPLICATION NUMBER: 60/229, 443

PRIOR FILING DATE: 2000 09 01

PRIOR APPLICATION NUMBER: 60/229, 445

PRIOR FILING DATE: 2000 09 01

PRIOR APPLICATION NUMBER: 60/229, 287

PRIOR FILING DATE: 2000 09 01

Mon Feb 3 11:23:16 2003

us-09-875-076-20.rapb

Page 11

Search completed: February 27, 2003, 08:08:24
List time: 18 secs

Database version 5.1.3
Copyright (c) 1994-2003 Computer Ltd.

EM protein protein search, using SW model

Run on: February 2, 2003, 02:02:45 : Search time 73 seconds

(without alignment) :
1092,816 Million cost, updates/sec

Hit list: 08:09 875 076-20

Footprint scores: 1992
Sequence: 1 MMTIDEPEVSNALSPSSA.....HAWWELGCAALPKEVVM 474

Scoring table:

gapop 10.0, capex 0.5

Search: 6/1580 seqs, 206047115 results

Total number of hits satisfying chosen parameters: 6/1580

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post processing: Minimum Match 100%

Listed first 40 summaries

Database:

1: SP_ARCHA: *
2: SP_BACTERIA: *
3: SP_FUNGI: *
4: SP_PLANTA: *
5: SP_INVERTEBRATA: *
6: SP_MAMMAL: *
7: SP_MURIC: *
8: SP_ORNITHO: *
9: SP_PHARO: *
10: SP_PLAT: *
11: SP_PODON: *
12: SP_VIRUS: *
13: SP_VERTICILL: *
14: SP_UNCLASSIFIED: *
15: SP_VIRUS: *
16: SP_BACTERIAP: *
17: SP_ARCHAOP: *

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|--------|--------------------|
| 1 | 270.5 | 13.6 | 456 | Q611Y4 | Q611Y4 ap1s mel111 |
| 2 | 269 | 13.5 | 48 | Q60K89 | Q60K89 mos mel111 |
| 3 | 263.5 | 12.7 | 499 | Q14167 | Q14167 homo sapien |
| 4 | 263.5 | 12.7 | 471 | Q96W77 | Q96W77 citreofiliu |
| 5 | 251 | 12.5 | 504 | Q9VX88 | Q9VX88 drosophila |
| 6 | 246 | 12.3 | 476 | Q96J36 | Q96J36 homo sapien |
| 7 | 243 | 12.2 | 470 | P97842 | P97842 rat1s nov |
| 8 | 242.5 | 12.2 | 447 | Q16144 | Q16144 homo sapien |
| 9 | 242.5 | 12.2 | 774 | Q9VAA2 | Q9VAA2 drosophila |
| 10 | 241 | 12.1 | 515 | Q9NKK7 | Q9NKK7 homo sapien |
| 11 | 240.5 | 12.1 | 508 | Q9VW23 | Q9VW23 homo sapien |
| 12 | 240 | 12.0 | 499 | Q9N302 | Q9N302 ap1s mel111 |
| 13 | 236.5 | 11.9 | 494 | Q9N4S6 | Q9N4S6 ap1ysia kut |
| 14 | 235.5 | 11.8 | 466 | Q9WY01 | Q9WY01 homo sapien |
| 15 | 235.5 | 11.8 | 474 | Q9WXX9 | Q9WXX9 homo sapien |
| 16 | 235.5 | 11.8 | 414 | Q9CKA0 | Q9CKA0 canis fami |

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|----|-------|------|-----|---------|---------------------|
| 17 | 235.5 | 11.8 | 474 | Q9CK99 | Q9CK99 canis fami |
| 18 | 235.5 | 11.8 | 447 | Q9SKH2 | Q9SKH2 sus scr114 |
| 19 | 234.5 | 11.8 | 532 | Q17496 | Q17496 ascaris son |
| 20 | 234 | 11.7 | 496 | Q9Z492 | Q9Z492 homo sapien |
| 21 | 234 | 11.7 | 471 | Q98D08 | Q98D08 tot1aobn 1 |
| 22 | 233.5 | 11.7 | 408 | Q98998 | Q98998 xenopus lae |
| 23 | 232.5 | 11.7 | 450 | Q987K1 | Q987K1 homo sapien |
| 24 | 231.5 | 11.6 | 374 | Q42342 | Q42342 cytol1us ca |
| 25 | 231.5 | 11.6 | 510 | Q908Y5 | Q908Y5 brachydrilo |
| 26 | 230 | 11.5 | 422 | Q9N298 | Q9N298 pan troglod |
| 27 | 229.5 | 11.5 | 494 | Q9NH35 | Q9NH35 cytol1us cal |
| 28 | 229 | 11.5 | 422 | Q9N296 | Q9N296 puma puma |
| 29 | 228 | 11.4 | 422 | Q9N297 | Q9N297 act11a for |
| 30 | 227 | 11.4 | 406 | Q70824 | Q70824 homo sapien |
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| 33 | 226.5 | 11.4 | 429 | Q98203 | Q98203 cytol1us cal |
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| 35 | 226.5 | 11.4 | 466 | Q96R88 | Q96R88 homo sapien |
| 36 | 225.5 | 11.3 | 465 | Q9N239 | Q9N239 pan troglod |
| 37 | 225.5 | 11.3 | 440 | Q9N244 | Q9N244 canis fami |
| 38 | 225 | 11.3 | 683 | Q17476 | Q17476 carobabacti |
| 39 | 224.5 | 11.3 | 465 | Q9E204 | Q9E204 homo sapien |
| 40 | 224 | 11.2 | 443 | Q9G101 | Q9G101 canis fami |
| 41 | 223.5 | 11.2 | 455 | Q91A35 | Q91A35 trophila 41 |
| 42 | 223.5 | 11.2 | 405 | Q9C882 | Q9C882 mos musculu |
| 43 | 222.5 | 11.2 | 465 | Q9N208 | Q9N208 act11a for |
| 44 | 222.5 | 11.2 | 465 | Q9N207 | Q9N207 puma puma |
| 45 | 222.5 | 11.2 | 372 | 1879945 | 1879945 xenopus lae |

ATTENTIONS

| | | | | |
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| RESULT 1 | | | | |
| ID | Q610Y4 | PRELIMINARY: | PR1: | 456 AA. |
| AC | Q610Y4: | | | |
| DT | 01-JUN-2002 (TREMUR): 21, (revised) | | | |
| DT | 01-JUN-2002 (TREMUR): 21, (last sequence update) | | | |
| DT | 01-JUN-2002 (TREMUR): 21, (last annotation update) | | | |
| DE | Depanline receptor type 1-2; | | | |
| GN | dep2. | | | |
| OS | Ap1s mell111 (Drosophy). | | | |
| OC | Inkayotai; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; | | | |
| OC | Ap1ysia; Mesoptera; Euphydryinae; Hymenoptera; Acetab; Aculeata; | | | |
| OC | Ap1obact; Apidae; Apis. | | | |
| OX | NCBI TaxID:7460; | | | |
| KN | (1) | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RC | TISSUE-BRAIN MUSCLEOM 60185; | | | |
| KA | MELLINE-96194783; PubMed 9535160; | | | |
| KA | Elect P.R.; Rowland J.E.; 1 and 11 P. | | | |
| RI | Isolation of seven unique cDNA clones from the | | | |
| RI | honey bee by library screening. | | | |
| RL | Insect Mol. Biol. 7:151-162(1990). | | | |
| KN | (2) | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RC | TISSUE-BRAIN MUSCLEOM 60185; | | | |
| KA | Humphries M.A.; Mustard J.; Hunter S.J.; Mercer A.; Ward V. | | | |
| KA | Elect P.R.; | | | |
| RI | "An invertebrate U2 type depanline receptor exhibits plasticity of | | | |
| RI | expression in the mushroom bodies of the honey bee brain reprogramed | | | |
| RI | with 16-day larval maturation of adults." | | | |
| RI | Submitted (Apr-2002) to the EMBL/Genbank/NCBI databases. | | | |
| DR | EMBL: A749806; AAM19330.1; | | | |
| KW | Keywords: | | | |
| SO | SEQUENCE: 456 AA; 5209 MW; 44662547086370A Cn694; | | | |
| Query Match | 13.6% | Score 270.5; | DB 5; | Length 456; |
| Host Local Similarity | 24.0%; | Prod. No. 16-17; | | |
| Matches | 89; | Conservative | 62; | Mismatches 164; |
| | | | Indels | 44; |
| | | | Gaps | 11; |

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[illegible][illegible]

[illegible][illegible][illegible]

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| 07 | 5 | 17 PVEFLDITLALGILSAAVPEPLVASPKHSSWHSLSAKVIALMAVETPILALMLPS | 116 | | |
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| 07 | 11 | 17 ISVYRYMALAH | HRVYAKMLTWAAV | CMWLTLSAMALPEVE | 100 |
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| 07 | 16 | 16 DWTLEKFLPEEHW | LEHHYFKAN | LLGLMLMAVIMAAHNAVYKLLLEHYHKK | 216 |
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| 10 | 18 | 18 HRYVAHEEYNNVETLNASLEPEETPEPVSLEPENSLEY | INLEKRLKI | 241 | |
| 07 | 21 | 217 KRIWQKRVALNSDMLTHGVALIGUAAANMLVHGRHMLTLLSLTGNHMAASRGLDMD | 276 | | |
| 10 | 24 | 242 KLLGALHFAA | MEHTEFAQS | LDPLDQWDLWGRKHGEMTL | 272 |
| 07 | 27 | 272 EVKAGKAGRMVYALDLLEPLWSPYVAWYMKVKAFAVHERVAVIWMHSTALAAVN | 306 | | |
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| 10 | 27 | 274 HRRVAKSLAVVSTGLD | WAVYTLMLTRAGTLP | VLYVYVEISLWLLWANSAYN | 428 |
| 07 | 44 | 447 DLVVTLKRLK | KQTL | 452 | |
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| 10 | 42 | 429 PVLYPTJHSEKAF | 444 | | |

Search completed: February 2, 2005, 04:41:02
Job: 1300 - 77 Sequ

1. $\frac{1}{2}$ 2. $\frac{1}{3}$ 3. $\frac{1}{4}$ 4. $\frac{1}{5}$ 5. $\frac{1}{6}$ 6. $\frac{1}{7}$ 7. $\frac{1}{8}$ 8. $\frac{1}{9}$ 9. $\frac{1}{10}$ 10. $\frac{1}{11}$ 11. $\frac{1}{12}$ 12. $\frac{1}{13}$ 13. $\frac{1}{14}$ 14. $\frac{1}{15}$ 15. $\frac{1}{16}$ 16. $\frac{1}{17}$ 17. $\frac{1}{18}$ 18. $\frac{1}{19}$ 19. $\frac{1}{20}$ 20. $\frac{1}{21}$ 21. $\frac{1}{22}$ 22. $\frac{1}{23}$ 23. $\frac{1}{24}$ 24. $\frac{1}{25}$ 25. $\frac{1}{26}$ 26. $\frac{1}{27}$ 27. $\frac{1}{28}$ 28. $\frac{1}{29}$ 29. $\frac{1}{30}$ 30. $\frac{1}{31}$ 31. $\frac{1}{32}$ 32. $\frac{1}{33}$ 33. $\frac{1}{34}$ 34. $\frac{1}{35}$ 35. $\frac{1}{36}$ 36. $\frac{1}{37}$ 37. $\frac{1}{38}$ 38. $\frac{1}{39}$ 39. $\frac{1}{40}$ 40. $\frac{1}{41}$ 41. $\frac{1}{42}$ 42. $\frac{1}{43}$ 43. $\frac{1}{44}$ 44. $\frac{1}{45}$ 45. $\frac{1}{46}$ 46. $\frac{1}{47}$ 47. $\frac{1}{48}$ 48. $\frac{1}{49}$ 49. $\frac{1}{50}$ 50. $\frac{1}{51}$ 51. $\frac{1}{52}$ 52. $\frac{1}{53}$ 53. $\frac{1}{54}$ 54. $\frac{1}{55}$ 55. $\frac{1}{56}$ 56. $\frac{1}{57}$ 57. $\frac{1}{58}$ 58. $\frac{1}{59}$ 59. $\frac{1}{60}$ 60. $\frac{1}{61}$ 61. $\frac{1}{62}$ 62. $\frac{1}{63}$ 63. $\frac{1}{64}$ 64. $\frac{1}{65}$ 65. $\frac{1}{66}$ 66. $\frac{1}{67}$ 67. $\frac{1}{68}$ 68. $\frac{1}{69}$ 69. $\frac{1}{70}$ 70. $\frac{1}{71}$ 71. $\frac{1}{72}$ 72. $\frac{1}{73}$ 73. $\frac{1}{74}$ 74. $\frac{1}{75}$ 75. $\frac{1}{76}$ 76. $\frac{1}{77}$ 77. $\frac{1}{78}$ 78. $\frac{1}{79}$ 79. $\frac{1}{80}$ 80. $\frac{1}{81}$ 81. $\frac{1}{82}$ 82. $\frac{1}{83}$ 83. $\frac{1}{84}$ 84. $\frac{1}{85}$ 85. $\frac{1}{86}$ 86. $\frac{1}{87}$ 87. $\frac{1}{88}$ 88. $\frac{1}{89}$ 89. $\frac{1}{90}$ 90. $\frac{1}{91}$ 91. $\frac{1}{92}$ 92. $\frac{1}{93}$ 93. $\frac{1}{94}$ 94. $\frac{1}{95}$ 95. $\frac{1}{96}$ 96. $\frac{1}{97}$ 97. $\frac{1}{98}$ 98. $\frac{1}{99}$ 99. $\frac{1}{100}$ 100. $\frac{1}{101}$ 101. $\frac{1}{102}$ 102. $\frac{1}{103}$ 103. $\frac{1}{104}$ 104. $\frac{1}{105}$ 105. $\frac{1}{106}$ 106. $\frac{1}{107}$ 107. $\frac{1}{108}$ 108. $\frac{1}{109}$ 109. $\frac{1}{110}$ 110. $\frac{1}{111}$ 111. $\frac{1}{112}$ 112. $\frac{1}{113}$ 113. $\frac{1}{114}$ 114. $\frac{1}{115}$ 115. $\frac{1}{116}$ 116. $\frac{1}{117}$ 117. $\frac{1}{118}$ 118. $\frac{1}{119}$ 119. $\frac{1}{120}$ 120. $\frac{1}{121}$ 121. $\frac{1}{122}$ 122. $\frac{1}{123}$ 123. $\frac{1}{124}$ 124. $\frac{1}{125}$ 125. $\frac{1}{126}$ 126. $\frac{1}{127}$ 127. $\frac{1}{128}$ 128. $\frac{1}{129}$ 129. $\frac{1}{130}$ 130. $\frac{1}{131}$ 131. $\frac{1}{132}$ 132. $\frac{1}{133}$ 133. $\frac{1}{134}$ 134. $\frac{1}{135}$ 135. $\frac{1}{136}$ 136. $\frac{1}{137}$ 137. $\frac{1}{138}$ 138. $\frac{1}{139}$ 139. $\frac{1}{140}$ 140. $\frac{1}{141}$ 141. $\frac{1}{142}$ 142. $\frac{1}{143}$ 143. $\frac{1}{144}$ 144. $\frac{1}{145}$ 145. $\frac{1}{146}$ 146. $\frac{1}{147}$ 147. $\frac{1}{148}$ 148. $\frac{1}{149}$ 149. $\frac{1}{150}$ 150. $\frac{1}{151}$ 151. $\frac{1}{152}$ 152. $\frac{1}{153}$ 153. $\frac{1}{154}$ 154. $\frac{1}{155}$ 155. $\frac{1}{156}$ 156. $\frac{1}{157}$ 157. $\frac{1}{158}$ 158. $\frac{1}{159}$ 159. $\frac{1}{160}$ 160. $\frac{1}{161}$ 161. $\frac{1}{162}$ 162. $\frac{1}{163}$ 163. $\frac{1}{164}$ 164. $\frac{1}{165}$ 165. $\frac{1}{166}$ 166. $\frac{1}{167}$ 167. $\frac{1}{168}$ 168. $\frac{1}{169}$ 169. $\frac{1}{170}$ 170. $\frac{1}{171}$ 171. $\frac{1}{172}$ 172. $\frac{1}{173}$ 173. $\frac{1}{174}$ 174. $\frac{1}{175}$ 175. $\frac{1}{176}$ 176. $\frac{1}{177}$ 177. $\frac{1}{178}$ 178. $\frac{1}{179}$ 179. $\frac{1}{180}$ 180. $\frac{1}{181}$ 181. $\frac{1}{182}$ 182. $\frac{1}{183}$ 183. $\frac{1}{184}$ 184. $\frac{1}{185}$ 185. $\frac{1}{186}$ 186. $\frac{1}{187}$ 187. $\frac{1}{188}$ 188. $\frac{1}{189}$ 189. $\frac{1}{190}$ 190. $\frac{1}{191}$ 191. $\frac{1}{192}$ 192. $\frac{1}{193}$ 193. $\frac{1}{194}$ 194. $\frac{1}{195}$ 195. $\frac{1}{196}$ 196. $\frac{1}{197}$ 197. $\frac{1}{198}$ 198. $\frac{1}{199}$ 199. $\frac{1}{200}$ 200. $\frac{1}{201}$ 201. $\frac{1}{202}$ 202. $\frac{1}{203}$ 203. $\frac{1}{204}$ 204. $\frac{1}{205}$ 205. $\frac{1}{206}$ 206. $\frac{1}{207}$ 207. $\frac{1}{208}$ 208. $\frac{1}{209}$ 209. $\frac{1}{210}$ 210. $\frac{1}{211}$ 211. $\frac{1}{212}$ 212. $\frac{1}{213}$ 213. $\frac{1}{214}$ 214. $\frac{1}{215}$ 215. $\frac{1}{216}$ 216. $\frac{1}{217}$ 217. $\frac{1}{218}$ 218. $\frac{1}{219}$ 219. $\frac{1}{220}$ 220. $\frac{1}{221}$ 221. $\frac{1}{222}$ 222. $\frac{1}{223}$ 223. $\frac{1}{224}$ 224. $\frac{1}{225}$ 225. $\frac{1}{226}$ 226. $\frac{1}{227}$ 227. $\frac{1}{228}$ 228. $\frac{1}{229}$ 229. $\frac{1}{230}$ 230. $\frac{1}{231}$ 231. $\frac{1}{232}$ 232. $\frac{1}{233}$ 233. $\frac{1}{234}$ 234. $\frac{1}{235}$ 235. $\frac{1}{236}$ 236. $\frac{1}{237}$ 237. $\frac{1}{238}$ 238. $\frac{1}{239}$ 239. $\frac{1}{240}$ 240

$$\mathcal{L}_{\text{reg}}(\mathbf{w}) = \frac{1}{2} \|\mathbf{w}\|_2^2$$

M. F. C. O'Leary - Review of "Using Sex Models"

KEYWORDS: *Healthcare; Ethics; Leadership; Management; Nursing; Quality Improvement; Simulation; Systems Thinking; Training; Workforce Development*

(With four additional updates) 773, 544 Million updates/sec

1175-176, 200

87-176-2

MANITOWOC STEEL CO. MANITOWOC STEEL CO. 474

References

$$f(x) = \begin{cases} 1 & \text{if } x \in \mathbb{Q} \\ 0 & \text{if } x \notin \mathbb{Q} \end{cases}$$
[illegible]

Journal of Interpersonal Violence 28(15)

1. $\mathcal{M} = \{M_1, M_2, \dots, M_n\}$ is a set of n matrices, where M_i is an $n \times n$ matrix.

Maximalist vs. Minimalist

$$E_{\text{eff}} = \frac{1}{2} \left(\frac{1}{E_1} + \frac{1}{E_2} \right) \quad \text{for } E_1 \neq E_2$$

Maximilian Maitz (1963)

[illegible][illegible]

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARY

| Genus | Species | Year | Locality | Length | Wing | Tail | Tarsus | Middle toe | Weight | Sex | Age | Remarks |
|-------|---------|------|----------|--------|------|-------|--------|------------|--------|-----|-----|---------|
| 1 | 1986 | 99.7 | 474 | 1 | SRK3 | HUMAN | | | | | | |
| 2 | 1975 | 99.1 | 474 | 1 | SRK3 | KAI | | | | | | |
| 3 | 1975 | 81.6 | 487 | 1 | SRK3 | BRABE | | | | | | |
| 4 | 1988 | 64.7 | 487 | 1 | SRK3 | HUMAN | | | | | | |
| 5 | 1988 | 54.7 | 471 | 1 | SRK3 | BRABE | | | | | | |
| 6 | 1981 | 51.8 | 375 | 1 | SRK3 | HUMAN | | | | | | |
| 7 | 1923 | 51.4 | 377 | 1 | SRK3 | KAI | | | | | | |
| 8 | 1922 | 51.3 | 379 | 1 | SRK3 | MOUSE | | | | | | |
| 9 | 269.5 | 43.5 | 470 | 1 | SRK3 | KAI | | | | | | |
| 10 | 264 | 43.4 | 387 | 1 | SRK3 | MOUSE | | | | | | |
| 11 | 260 | 43.4 | 400 | 1 | SRK3 | HUMAN | | | | | | |
| 12 | 259.5 | 43.0 | 471 | 1 | SRK3 | KAI | | | | | | |
| 13 | 259.5 | 43.0 | 471 | 1 | SRK3 | MOUSE | | | | | | |
| 14 | 259.5 | 43.0 | 471 | 1 | SRK3 | MOUSE | | | | | | |
| 15 | 259.5 | 43.0 | 471 | 1 | SRK3 | KAI | | | | | | |
| 16 | 257 | 42.9 | 471 | 1 | SRK3 | HUMAN | | | | | | |
| 17 | 256.5 | 42.9 | 539 | 1 | SRK3 | MOUSE | | | | | | |
| 18 | 256 | 42.9 | 487 | 1 | SRK3 | KAI | | | | | | |
| 19 | 256 | 42.9 | 400 | 1 | SRK3 | BRABE | | | | | | |
| 20 | 251 | 42.6 | 467 | 1 | SRK3 | BRABE | | | | | | |
| 21 | 251.5 | 42.6 | 454 | 1 | SRK3 | CANIA | | | | | | |
| 22 | 247 | 42.4 | 452 | 1 | SRK3 | KAI | | | | | | |
| 23 | 245 | 42.4 | 436 | 1 | SRK3 | MOUSE | | | | | | |
| 24 | 244 | 42.2 | 448 | 1 | SRK3 | HUMAN | | | | | | |
| 25 | 243.5 | 42.2 | 447 | 1 | SRK3 | KAI | | | | | | |
| 26 | 241.5 | 42.2 | 448 | 1 | SRK3 | KAI | | | | | | |
| 27 | 241.5 | 42.1 | 446 | 1 | SRK3 | BRABE | | | | | | |
| 28 | 241 | 42.0 | 445 | 1 | SRK3 | BRABE | | | | | | |
| 29 | 241.5 | 42.0 | 467 | 1 | SRK3 | KAI | | | | | | |
| 30 | 247 | 41.9 | 446 | 1 | SRK3 | KAI | | | | | | |
| 31 | 247 | 41.9 | 454 | 1 | SRK3 | HUMAN | | | | | | |
| 32 | 247 | 41.9 | 479 | 1 | SRK3 | KAI | | | | | | |
| 33 | 247 | 41.9 | 504 | 1 | SRK3 | BRABE | | | | | | |

天竺五、二五、一

| ID | SYMBOL/HUMAN | STANDARD | PROT | 474 AA |
|----|--|----------|------|--------|
| AA | Q7NS66 | | | |
| 24 | 15-OCT-2001 (Ref. 4); (Updated) | | | |
| 24 | 15-OCT-2001 (Ref. 4); Last sequence update) | | | |
| 24 | 15-JUN-2002 (Ref. 4); Last annotation update) | | | |
| 24 | Short conserved receptor expressed in brain A. SHERA. | | | |
| 25 | From SAPTons (Human): | | | |
| 25 | Eukaryotic Metazoa: Chordata: Vertebrata: Vertebrata: Mammalia: Eutheria: Primates: Catarrhini: Hominoidea: Hominidae: Homo. | | | |
| 25 | NCBI_Locus 9666: | | | |
| 25 | 111 | | | |
| 25 | Sequence from N.A. | | | |
| 25 | 11506 brain: | | | |
| 25 | MEHLIN 20294882; PubMed 1663454; | | | |
| 25 | Marumoto M., Saito T., Takasaki T., Kamohara M., Sugimoto T., Kobayashi M., Tadokoro M., Matsunoto S., Ohishi T., Fushimi K., | | | |
| 25 | "An evolutionarily conserved G-protein-coupled receptor family, SHERA, expressed in the central nervous system." | | | |
| 25 | Brochem. Biophys. Res. Commun. 272:576-582(2000). | | | |
| 25 | 121 | | | |
| 25 | Sequence from N.A. | | | |
| 25 | 11506 brain: | | | |
| 25 | Submitted (101-2001) to the EMBL/Genbank/NCBI databases. | | | |
| 25 | 1-1 FUNCTION: ORIGIN RECEPTOR. | | | |
| 25 | 1-1 SUBCELLULAR LOCATION: Integral membrane protein (by similarity). | | | |
| 25 | 1-1 TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVELS IN BRAIN AND OVARY. | | | |
| 25 | 1-1 LOWER LEVELS IN SMALL INTESTINE, IN BRAIN REGIONS, DETECTED IN ALL REGIONS TESTED. HIGHEST LEVELS IN THE CEREBELLUM AND CEREBRAL CORTEX. | | | |
| 25 | 1-1 SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS. | | | |
| 25 | 1-1 THIS SWISS PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL station in the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed, misused by and for commercial entities requires a license agreement (see http://www.isb.scrib.ac.uk/ or send an email to license@sb.scrib.ac.uk). | | | |
| 25 | EMBL: AB040801; F0456647.1; | | | |
| 25 | EMBL: H009461; AA009461.1; | | | |
| 25 | MM: 400253; | | | |
| 25 | InterPro: IP000276; GPCR_kbdpsm. | | | |
| 25 | 11506 brain: 7101.1; 1. | | | |
| 25 | PRINIS: PR00237; GPCRkbdb-psn | | | |
| 25 | 16-05-15: PS00237; G-PROTEIN-RECEP_F1_1; FALSE NEG. | | | |
| 25 | 16-05-15: PS0262; G-PROTEIN-RECEP_F1_2; 1. | | | |
| 25 | G-Protein-coupled receptor; Transmembrane; Glycoprotein; Multigene family. | | | |
| 25 | 11506 brain: 26 | | | |
| 25 | TRANSFORM 27 47 EXONEXON:00AR (P-00EN10A) | | | |
| 25 | 11506 brain: 48 59 1 (P-00EN10A). | | | |
| 25 | 11506 brain: 48 59 1 (P-00EN10A). | | | |

Genbank version 5.1.1
Copyright (c) 1994 Zou's Computer Ltd.

MM protein protein search, using SW model

Ref: 001 February 2, 2003, 02:59:00 : Search time: 48 seconds

(with all updates/sec
944,645, 11,130, 001, 001, 001, 001)

Hit: 05 to 875-076-20

Ref: 001

Sequence: 1 MAMTGPDEPVSSALSPSSA.....HAWVWTRCAAPREYVM 473

Search: 001

Gap: 10.0 : 10.0 : 10.0

Score: 28424

Local: 28424

Maximum DB: 200000000

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1b 14 VIVRRKWO-----DQGLLAAWLLSAVASVVSRLNVPQ RQAAVQVLENGYVV 189
 1b 145 ANDLLEHMLAVLMAALHAAYGKILLEE YRHKRM ---KIVAVVATLSMMLEHDP 235
 1b 146 YSSVSTSELEEDHEMLTYWALTEKLLPHEWAKHKLHSHAKRP ---SDP 246
 1b 246 CATVGAANNLADPGRHM -PEELGTR 262
 1b 247 GPP-----VSQVGFEEHPPPLSLSLSTSSSSRPSSELSQRP SPPVLAAL 289
 1b 248 QNHASRKLMDQVKGKQKALHMEYALITLLMSPYLVACYWVWVAVVAPRY 421
 1b 249 PVPPESSRRRRGKTLDRERKRVPLVAVVAVLVWTFEYVHLLKADVAVSRK 349
 1b 422 LATAVWSTFAAANNVWVTLNKLK 448
 1b 450 VSAVWLVVNSALNPITYITFNAPR 476

RESULT 5

45 Depanline receptor - human
 C Species: Homo sapiens (man)
 C Date: 21-Dec-1999 #sequence_revision 05-Jun-1997 #text_change 14-Aug-1999
 C Accession: G01977
 RefSeqID: C82707, B, submitted to the EMBL Data Library, July 1995
 A Accession number: G01977
 A Status: preliminary; translated from cDNA/EMBL/GenBank
 A Molecular type: mRNA
 A residues: 1-400-PTS-
 A Cross-reference: EMBL:054499; NID:0927341; PIDD:AA47492.1; PIDD:0927342
 C Superfamily: vertebrate thapsin

Query Match 14.18; Score 260; 108 Z; Length 400;
 Post local similarity 24.08; Pred. No. 4, 20-16;
 Matches 94; Conservative 71; Mismatches 160; Indels 94; Gaps 14;

1b 4 NIDHEFVSALSPSSAAVYKVLGLIMVSLANALSLVLRKALHKAIVYPL 62
 1b 12 NITCAENSTGASQARHAYVALSYALIAL VESGLWGMVLEKALVTLNIVV 69
 1b 63 DGLTAGKSAVPEVYASVHSHSSTFSAISKIVANMAVETFKAKMPELSVRY 122
 1b 70 SLAVMLAVATLVMPVYVETGVWNSKIDVETLVIMMLASLMLALSHRY 129
 1b 123 MAI - AHREYAKRNIITGCAAVTGMWTSVAMAPPVETVCTKPLPEPDQTEFHR 179
 1b 140 LAVWGVVRYEETIGSSVGRVALMLFAVWLAFAVSTLLDPNT---KIDVLSISN 186
 1b 140 YKKA-NIDLEHMLAVLMAALHAAYGKILFEYRHRK-----MKP----- 219
 1b 187 DEVTSSVSVSPYDPGV -FLVYAKIYVVKGRKKKILHGNSSVSVGRFPQV 242
 1b 240 -----VAMVATLSNMIEHFGATGGAANNIACTGRDMDTL -LATRG- 263
 1b 248 LSPDPAHLEKRYSTVQVLAQMGPPGRDTEKREKLNLSSTFAKRLSEVERKS 302
 1b 248 NHAASRKLMDQVKGKQKALHMEYALITLLMSPYLVACYWVWVAVVAPRY 421
 1b 303 NGLSTSLKTLDLPGRVPLRRKAAQVAVLVDAETVWLLPPIHVLNIDVQVHVS 462
 1b 450 HRYLATAVWSTFAAANNVWVTLNKLK 457
 1b 450 ELYSAI TWGVNSALNPITYITFNHPRKFLKLSK 400

RESULT 6
 S02011
 Secretin receptor 2 rat
 N Amino acid residues: 5-hydroxytryptamine receptor 2 (5-HT2)

C Species: ratus norvegicus (Norway rat)
 C Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 14-Aug-1999
 C Accession: S02011
 RefSeqID: D.B.2, Barb. A.W.42, Wooley, M.; Talbot, C.C. 1981; Stock
 EMBL: J. 7, 415-4140, 1988
 A Title: Structure and functional expression of cloned rat secretin cDNA 2 receptor
 A Accession number: S02011; M01009210797; P010265454
 A Reference: S02011
 A Molecular type: mRNA
 A residues: 1-449-SPK-
 A Cross-reference: EMBL:014971; NID:057856; PIDD:AA42550.1; PIDD:057856
 C Superfamily: vertebrate thapsin
 C Keywords: G protein-coupled receptor; transmembrane protein

Query Match 14.08; Score 270.5; 108 Z; Length 449;
 Post local similarity 24.48; Pred. No. 40-16;
 Matches 90; Conservative 68; Mismatches 150; Indels 61; Gaps 14;

1b 17 PYSASAVKL ---VLATLMVSLACNALLSLVLRKALHKAIVYPLLDVLA 44
 1b 40 PPLSLSLHGRKWSALITLVITLACNLLVMAVSLERKLNATNFMSLALAM 99
 1b 70 IRSAVPEPVYASVHSHSSTFSAISKIVAFMAVETFAAALMDPELSYRRPAA 126
 1b 100 LDPVMPVSMITLLVYMPVLSKIDVETLVIMMLASLMLALSHRY 129
 1b 127 HIREYAKRNIITGCAAVTGMWTSVAMAPPVETVCTKPLPEPDQTEFHR 179
 1b 160 HSHPSKIKALTKLAV -WLSVLSMDLVETGLDPSVVRKSLANIVL 211
 1b 184 NIDLEHMLAVLMAALHAAYGKILFE -YRHKRMQVQVP -ATSGMTEH 235
 1b 216 GSEVAFETVETLVWVLYPLKSLKRALVCSVLSFKALSPSLVSSSKSLK 278
 1b 234 GPEATGGAANNVWVETVCTKPLPEPDQTEFHR 291
 1b 274 -----GRST-----KRGSSVAGRRDWSISNPKAKVATVTF- 308
 1b 292 TLFLHLSYIVACYVYK-AG--AVHRYATAVWSTFAAANNVWVTLNKLK 448
 1b 309 --EYVWVCTEFLNMAVLRKSNVNVGALLNFWVLYVYSSAVNIVYITNKR 456
 1b 449 KLTTHAV 457
 1b 467 SAESEYVQ 475

RESULT 7

5-hydroxytryptamine 2 receptor - mouse
 C Species: Mus musculus (house mouse)
 C Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 14-Aug-1999
 C Accession: S40689
 RefSeq: W. Chen, K. Jan, N.C. Gallagher, T.K. Shih, J.C.
 J. Neurosci. Res. 43, 196-204, 1992
 A Title: Gene structure and expression of the mouse 5-HT2 receptor
 A Accession number: S40689; M01004085774; P010244568
 A Molecular type: mRNA
 A residues: 1-471-VAN-
 A Cross-reference: EMBL:084542; NID:04261074; PIDD:AA42469.1; PIDD:04261075
 C Superfamily: vertebrate thapsin
 C Keywords: G protein-coupled receptor; transmembrane protein

Query Match 14.08; Score 259.5; 108 Z; Length 471;
 Post local similarity 24.18; Pred. No. 4, 20-16;
 Matches 89; Conservative 69; Mismatches 150; Indels 61; Gaps 14;

1b 17 PYSASAVKL -----VLATLMVSLANALSLVLRKALHKAIVYPLLDVLA 44
 1b 42 PPLSLSLHGRKWSALITLVITLACNLLVMAVSLERKLNATNFMSLALAM 121

57 257 TLTLIRKNNHAASRELDRLQEVKDRQLQEMFVALTLTLTLWSYLVAVYWRVYKVA 416
 100 425 - - - - - AQAKLL - - - - - AKRKYRMLLVIVLFPMQQLVYSANLWRAFDRLQA 468
 57 417 VIKRYLALAV - - - - - WNSFQAQAVNPV - - - - - QILNKLQKKVLIHAWGIGFALVPRF 464
 100 409 - - - - - HRAISVNIISFDHLSVNSAVNPIVYVCFMHRKRWALDITAKC - - - - - QIRRP 418

RESULT 15

S66402

Secretin receptor 7 - mouse

Nucleotide number: 5-hydroxytryptamine 7 receptor (5HT₇)

Species: Mus musculus (house mouse)

Update: 06-Jan-1995 #sequence_revision: 06-Jan-1995 #text_change: 20-Apr-2000

#Accession: 148779; S66402

ReleaseDate: 01-Dec-1987; N: 100; K:

Mol. Weight: 44, 229-246, 1994

A11103 Molecular cloning of a mammalian secretin receptor that activates adenylyate cy

Accession number: 148779; MIM:604091; EMBL:804987

Accession: 148779

Accession: translated from cDNA/EMBL/DBEST

Accession: type: mRNA

Accession: 1-418 bases

Accession: EMBL:724977; NID:496586; EMBL:724977; EMBL:724977

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% CURRENT FILING DATE: 2001-01-17
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| Post-graduate | 99-556 | Period | No. 1-2 | | 1-11 | | |
| Mathematics | 5-11 | Examination | 2-2 | Minutiae | 2-2 | Index | 1-1 |
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| RESULT 4 | US/09/089/442-v5 |
| Supplement 45, Attribution US/09/089/442 | |
| Publication No. US2003001504VAT | |
| GENERAL INFORMATION | |
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| 2 TITLE OF INVENTION: Molecule Acids, Protocols, and Antidotes | |
| 3 FILE REFERENCE: 14708 | |
| 4 CURRENT APPLICATION NUMBER: US/09/089/442 | |
| 5 CURRENT FILING DATE: 2003 11 21 | |
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| 8 PREVIOUS APPLICATION NUMBER: 60/180,628 | |
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PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/249,214
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/249,297
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/242,400
PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: 60/241,242
PRIOR FILING DATE: 2000-09-08
PRIOR APPLICATION NUMBER: 60/242,081
PRIOR FILING DATE: 2000-09-08
PRIOR APPLICATION NUMBER: 60/242,080
PRIOR FILING DATE: 2000-09-08
PRIOR APPLICATION NUMBER: 60/241,414
PRIOR FILING DATE: 2000-09-08
PRIOR APPLICATION NUMBER: 60/241,244
PRIOR FILING DATE: 2000-09-08
PRIOR APPLICATION NUMBER: 60/244,064
PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: 60/244,064
PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: 60/249,945
PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: 60/249,947
PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: 60/242,499
PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: 60/242,401
PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: 60/241,808
PRIOR FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: 60/241,826
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/241,786
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/241,221
PRIOR FILING DATE: 2000-10-26
PRIOR APPLICATION NUMBER: 60/246,475
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: 60/241,246
PRIOR FILING DATE: 2000-09-08
PRIOR APPLICATION NUMBER: 60/244,045
PRIOR FILING DATE: 2000-09-14

Query Match 45,886, Score 514,69, Pgs 92, 1000th 7552

| Host | Host Subunit | Latency | 6S | 8S | 7S | Protein | Mol. Wt. | 10S | 11S | 12S | 13S | 14S | 15S | 16S | 17S | 18S | 19S | 20S | 21S | 22S | 23S | 24S | 25S | 26S | 27S | 28S | 29S | 30S | 31S | 32S | 33S | 34S | 35S | 36S | 37S | 38S | 39S | 40S | 41S | 42S | 43S | 44S | 45S | 46S | 47S | 48S | 49S | 50S | 51S | 52S | 53S | 54S | 55S | 56S | 57S | 58S | 59S | 60S | 61S | 62S | 63S | 64S | 65S | 66S | 67S | 68S | 69S | 70S | 71S | 72S | 73S | 74S | 75S | 76S | 77S | 78S | 79S | 80S | 81S | 82S | 83S | 84S | 85S | 86S | 87S | 88S | 89S | 90S | 91S | 92S | 93S | 94S | 95S | 96S | 97S | 98S | 99S | 100S | 101S | 102S | 103S | 104S | 105S | 106S | 107S | 108S | 109S | 110S | 111S | 112S | 113S | 114S | 115S | 116S | 117S | 118S | 119S | 120S | 121S | 122S | 123S | 124S | 125S | 126S | 127S | 128S | 129S | 130S | 131S | 132S | 133S | 134S | 135S | 136S | 137S | 138S | 139S | 140S | 141S | 142S | 143S | 144S | 145S | 146S | 147S | 148S | 149S | 150S | 151S | 152S | 153S | 154S | 155S | 156S | 157S | 158S | 159S | 160S | 161S | 162S | 163S | 164S | 165S | 166S | 167S | 168S | 169S | 170S | 171S | 172S | 173S | 174S | 175S | 176S | 177S | 178S | 179S | 180S | 181S | 182S | 183S | 184S | 185S | 186S | 187S | 188S | 189S | 190S | 191S | 192S | 193S | 194S | 195S | 196S | 197S | 198S | 199S | 200S | 201S | 202S | 203S | 204S | 205S | 206S | 207S | 208S | 209S | 210S | 211S | 212S | 213S | 214S | 215S | 216S | 217S | 218S | 219S | 220S | 221S | 222S | 223S | 224S | 225S | 226S | 227S | 228S | 229S | 230S | 231S | 232S | 233S | 234S | 235S | 236S | 237S | 238S | 239S | 240S | 241S | 242S | 243S | 244S | 245S | 246S | 247S | 248S | 249S | 250S | 251S | 252S | 253S | 254S | 255S | 256S | 257S | 258S | 259S | 260S | 261S | 262S | 263S | 264S | 265S | 266S | 267S | 268S | 269S | 270S | 271S | 272S | 273S | 274S | 275S | 276S | 277S | 278S | 279S | 280S | 281S | 282S | 283S | 284S | 285S | 286S | 287S | 288S | 289S | 290S | 291S | 292S | 293S | 294S | 295S | 296S | 297S | 298S | 299S | 300S | 301S | 302S | 303S | 304S | 305S | 306S | 307S | 308S | 309S | 310S | 311S | 312S | 313S | 314S | 315S | 316S | 317S | 318S | 319S | 320S | 321S | 322S | 323S | 324S | 325S | 326S | 327S | 328S | 329S | 330S | 331S | 332S | 333S | 334S | 335S | 336S | 337S | 338S | 339S | 340S | 341S | 342S | 343S | 344S | 345S | 346S | 347S | 348S | 349S | 350S | 351S | 352S | 353S | 354S | 355S | 356S | 357S | 358S | 359S | 360S | 361S | 362S | 363S | 364S | 365S | 366S | 367S | 368S | 369S | 370S | 371S | 372S | 373S | 374S | 375S | 376S | 377S | 378S | 379S | 380S | 381S | 382S | 383S | 384S | 385S | 386S | 387S | 388S | 389S | 390S | 391S | 392S | 393S | 394S | 395S | 396S | 397S | 398S | 399S | 400S | 401S | 402S | 403S | 404S | 405S | 406S | 407S | 408S | 409S | 410S | 411S | 412S | 413S | 414S | 415S | 416S | 417S | 418S | 419S | 420S | 421S | 422S | 423S | 424S | 425S | 426S | 427S | 428S | 429S | 430S | 431S | 432S | 433S | 434S | 435S | 436S | 437S | 438S | 439S | 440S | 441S | 442S | 443S | 444S | 445S | 446S | 447S | 448S | 449S | 450S | 451S | 452S | 453S | 454S | 455S | 456S | 457S | 458S | 459S | 460S | 461S | 462S | 463S | 464S | 465S | 466S | 467S | 468S | 469S | 470S | 471S | 472S | 473S | 474S | 475S | 476S | 477S | 478S | 479S | 480S | 481S | 482S | 483S | 484S | 485S | 486S | 487S | 488S | 489S | 490S | 491S | 492S | 493S | 494S | 495S | 496S | 497S | 498S | 499S | 500S | 501S | 502S | 503S | 504S | 505S | 506S | 507S | 508S | 509S | 510S | 511S | 512S | 513S | 514S | 515S | 516S | 517S | 518S | 519S | 520S | 521S | 522S | 523S | 524S | 525S | 526S | 527S | 528S | 529S | 530S | 531S | 532S | 533S | 534S | 535S | 536S | 537S | 538S | 539S | 540S | 541S | 542S | 543S | 544S | 545S | 546S | 547S | 548S | 549S | 550S | 551S | 552S | 553S | 554S | 555S | 556S | 557S | 558S | 559S | 560S | 561S | 562S | 563S | 564S | 565S | 566S | 567S | 568S | 569S | 570S | 571S | 572S | 573S | 574S | 575S | 576S | 577S | 578S | 579S | 580S | 581S | 582S | 583S | 584S | 585S | 586S | 587S | 588S | 589S | 590S | 591S | 592S | 593S | 594S | 595S | 596S | 597S | 598S | 599S | 600S | 601S | 602S | 603S | 604S | 605S | 606S | 607S | 608S | 609S | 610S | 611S | 612S | 613S | 614S | 615S | 616S | 617S | 618S | 619S | 620S | 621S | 622S | 623S | 624S | 625S | 626S | 627S | 628S | 629S | 630S | 631S | 632S | 633S | 634S | 635S | 636S | 637S | 638S | 639S | 640S | 641S | 642S | 643S | 644S | 645S | 646S | 647S | 648S | 649S | 650S | 651S | 652S | 653S | 654S | 655S | 656S | 657S | 658S | 659S | 660S | 661S | 662S | 663S | 664S | 665S | 666S | 667S | 668S | 669S | 670S | 671S | 672S | 673S | 674S | 675S | 676S | 677S | 678S | 679S | 680S | 681S | 682S | 683S | 684S | 685S | 686S | 687S | 688S | 689S | 690S | 691S | 692S | 693S | 694S | 695S | 696S | 697S | 698S | 699S | 700S | 701S | 702S | 703S | 704S | 705S | 706S | 707S | 708S | 709S | 710S | 711S | 712S | 713S | 714S | 715S | 716S | 717S | 718S | 719S | 720S | 721S | 722S | 723S | 724S | 725S | 726S | 727S | 728S | 729S | 730S | 731S | 732S | 733S | 734S | 735S | 736S | 737S | 738S | 739S | 740S | 741S | 742S | 743S | 744S | 745S | 746S | 747S | 748S | 749S | 750S | 751S | 752S | 753S | 754S | 755S | 756S | 757S | 758S | 759S | 760S | 761S | 762S | 763S | 764S | 765S | 766S | 767S | 768S | 769S | 770S | 771S | 772S | 773S | 774S | 775S | 776S | 777S | 778S | 779S | 780S | 781S | 782S | 783S | 784S | 785S | 786S | 787S | 788S | 789S | 790S | 791S | 792S | 793S | 794S | 795S | 796S | 797S | 798S | 799S | 800S | 801S | 802S | 803S | 804S | 805S | 806S | 807S | 808S | 809S | 810S | 811S | 812S | 813S | 814S | 815S | 816S | 817S | 818S | 819S | 820S | 821S | 822S | 823S | 824S | 825S | 826S | 827S | 828S | 829S | 830S | 831S | 832S | 833S | 834S | 835S | 836S | 837S | 838S | 839S | 840S | 841S | 842S | 843S | 844S | 845S | 846S | 847S | 848S | 849S | 850S | 851S | 852S | 853S | 854S | 855S | 856S | 857S | 858S | 859S | 860S | 861S | 862S | 863S | 864S | 865S | 866S | 867S | 868S | 869S | 870S | 871S | 872S | 873S | 874S | 875S | 876S | 877S | 878S | 879S | 880S | 881S | 882S | 883S | 884S | 885S | 886S | 887S | 888S | 889S | 890S | 891S | 892S | 893S | 894S | 895S | 896S | 897S | 898S | 899S | 900S | 901S | 902S | 903S | 904S | 905S | 906S | 907S | 908S | 909S | 910S | 911S | 912S | 913S | 914S | 915S | 916S | 917S | 918S | 919S | 920S | 921S | 922S | 923S | 924S | 925S | 926S | 927S | 928S | 929S | 930S | 931S | 932S | 933S | 934S | 935S | 936S | 937S | 938S | 939S | 940S | 941S | 942S | 943S | 944S | 945S | 946S | 947S | 948S | 949S | 950S | 951S | 952S | 953S | 954S | 955S | 956S | 957S | 958S | 959S | 960S | 961S | 962S | 963S | 964S | 965S | 966S | 967S | 968S | 969S | 970S | 971S | 972S | 973S | 974S | 975S | 976S | 977S | 978S | 979S | 980S | 981S | 982S | 983S | 984S | 985S | 986S | 987S | 988S | 989S | 990S | 991S | 992S | 993S | 994S | 995S | 996S | 997S | 998S | 999S | 1000S |
|------|--------------|---------|----|----|----|---------|----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|--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|------|--------------|---------|----|----|----|---------|----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|--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[illegible]

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|----|---|-------|-------------------|----------|--------------|
| 1 | STATE: Illinois | 7.98 | Score: 88.4 | DB: 1 | Length: 1370 |
| 2 | COUNTRY: USA | 40.48 | Prod. No: 7480-14 | | |
| 3 | ZIP: 60606 | 0 | Missed calls: 291 | Indis: 4 | Caps: 1 |
| 4 | COMPUTER READABLE FORM: | | | | |
| 5 | MEDIUM TYPE: Floppy disk | | | | |
| 6 | COMPIER: IBM PC compatible | | | | |
| 7 | OPERATING SYSTEM: PC DOS/MS DOS | | | | |
| 8 | SOFTWARE: Patient Release #1.0, Version #1.25 | | | | |
| 9 | CURRENT APPLICATION DATA: | | | | |
| 10 | APPLICATION NUMBER: US/08/056,051 | | | | |
| 11 | FILING DATE: 1990-04-29 | | | | |
| 12 | CLASSIFICATION: 435 | | | | |
| 13 | ATTORNEY/AGENT INFORMATION: | | | | |
| 14 | NAME: Mr. 5516681000, Kevin E | | | | |
| 15 | REGISTRATION NUMBER: 45,403 | | | | |
| 16 | REGISTRATION/BOOKLET NUMBER: 90,109,200 | | | | |
| 17 | TELECOMMUNICATION INFORMATION: | | | | |
| 18 | TELEPHONE: 312 715 1000 | | | | |
| 19 | TELEFAX: 312-715-1244 | | | | |
| 20 | TELEX: 910 221-5417 | | | | |
| 21 | INFORMATION FOR SEQ ID NO: 1: | | | | |
| 22 | SEQUENCE CHARACTERISTICS: | | | | |
| 23 | LENGTH: 1370 base pairs | | | | |
| 24 | TYPE: Nucleic Acid | | | | |
| 25 | STRANDNESS: Single- | | | | |
| 26 | Topology: linear | | | | |
| 27 | MOLWGT: 10000 | | | | |
| 28 | FEATURE: | | | | |
| 29 | NAME/KEY: 5'UTR | | | | |
| 30 | LOCATION: 1..103 | | | | |
| 31 | FEATURE: | | | | |
| 32 | NAME/KEY: 3'UTR | | | | |
| 33 | LOCATION: 1268..1370 | | | | |
| 34 | FEATURE: | | | | |
| 35 | NAME/KEY: CDS | | | | |
| 36 | LOCATION: 104..1267 | | | | |
| 37 | OS=08-056-051-1 | | | | |
| 38 | Genety Match | | | | |
| 39 | Host Local Simulation City | | | | |
| 40 | Missed calls: 258 | | | | |
| 41 | Missed calls: 258 | | | | |
| 42 | Missed calls: 258 | | | | |
| 43 | Missed calls: 258 | | | | |
| 44 | Missed calls: 258 | | | | |
| 45 | Missed calls: 258 | | | | |
| 46 | Missed calls: 258 | | | | |
| 47 | Missed calls: 258 | | | | |
| 48 | Missed calls: 258 | | | | |
| 49 | Missed calls: 258 | | | | |
| 50 | Missed calls: 258 | | | | |
| 51 | Missed calls: 258 | | | | |
| 52 | Missed calls: 258 | | | | |
| 53 | Missed calls: 258 | | | | |
| 54 | Missed calls: 258 | | | | |
| 55 | Missed calls: 258 | | | | |
| 56 | Missed calls: 258 | | | | |
| 57 | Missed calls: 258 | | | | |
| 58 | Missed calls: 258 | | | | |
| 59 | Missed calls: 258 | | | | |
| 60 | Missed calls: 258 | | | | |
| 61 | Missed calls: 258 | | | | |
| 62 | Missed calls: 258 | | | | |
| 63 | Missed calls: 258 | | | | |
| 64 | Missed calls: 258 | | | | |
| 65 | Missed calls: 258 | | | | |
| 66 | Missed calls: 258 | | | | |
| 67 | Missed calls: 258 | | | | |
| 68 | Missed calls: 258 | | | | |
| 69 | Missed calls: 258 | | | | |
| 70 | Missed calls: 258 | | | | |
| 71 | Missed calls: 258 | | | | |
| 72 | Missed calls: 258 | | | | |
| 73 | Missed calls: 258 | | | | |
| 74 | Missed calls: 258 | | | | |
| 75 | Missed calls: 258 | | | | |
| 76 | Missed calls: 258 | | | | |
| 77 | Missed calls: 258 | | | | |
| 78 | Missed calls: 258 | | | | |
| 79 | Missed calls: 258 | | | | |
| 80 | Missed calls: 258 | | | | |
| 81 | Missed calls: 258 | | | | |
| 82 | Missed calls: 258 | | | | |
| 83 | Missed calls: 258 | | | | |
| 84 | Missed calls: 258 | | | | |
| 85 | Missed calls: 258 | | | | |
| 86 | Missed calls: 258 | | | | |
| 87 | Missed calls: 258 | | | | |
| 88 | Missed calls: 258 | | | | |
| 89 | Missed calls: 258 | | | | |
| 90 | Missed calls: 258 | | | | |
| 91 | Missed calls: 258 | | | | |
| 92 | Missed calls: 258 | | | | |
| 93 | Missed calls: 258 | | | | |
| 94 | Missed calls: 258 | | | | |
| 95 | Missed calls: 258 | | | | |
| 96 | Missed calls: 258 | | | | |
| 97 | Missed calls: 258 | | | | |
| 98 | Missed calls: 258 | | | | |

[illegible]


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1  REFERENCE/WORK ITEM NUMBER: 3011394 MM
2  TELECOMMUNICATION INFORMATION:
3  TELEPHONE: 412 913 0001
4  TELEFAX: 412 913 0002
5  FEATURES:
6  INFORMATION FROM SEQ. IT NO.: 17;
7  SEQUENCE CHARACTERISTICS:
8  LENGTH: 1370 base pairs
9  TYPE: nucleic acid
10  STRANDEDNESS: single
11  topology: linear
12  molecule type: cDNA
13  FEATURES:
14  NAME/KEY: c01R
15  LOCATION: 1..1370
16  FEATURE:
17  NAME/KEY: c01R
18  LOCATION: 1..1370
19  FEATURE:
20  NAME/KEY: 1268..1370
21  FEATURE:
22  NAME/KEY: c05
23  LOCATION: 104..1267
24  DIS. 019-0606 6594-17

```


Sequencing is compared to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 ambiguities with a minimum of 2 clones and 4 reads with no ambiguities. If the sequence quality does not meet this standard, it will be indicated in the annotation.

The repeat regions shown were identified using RepeatMasker by Adrian Smith.

Sequence similarities were identified using Blastlast by J. Michael Zbind.

Exon/Intron boundaries of identified genes were chosen. If there were canonical splice junctions that maintained sequence continuity across the splice junctions:

```

FEATURES
    Source
        Location/Qualifiers
            1..56821
                /organism "Mus musculus"
                /db_xref "taxon:10090"
                /chromosome "X"
                /clone "RZ438215"
            423..493
                /rpt_family "CTD)n"
            764..805
                /rpt_family "CTD)n"
            2171..2222
                /rpt_family "MER4-internal"
            2223..2255
                /rpt_family "CTD)n"
            2825..2849
                /rpt_family "CTD)n"
            3522..3563
                /rpt_family "CTD)n"
            4016..4367
                /rpt_family "CTD)n"
            4550..4565
                /rpt_family "CTD)n"
            4677..4858
                /rpt_family "MIR"
            5742..5858
                /rpt_family "RS1M1"
            complement(5910..6099)
                /rpt_family "R1_MM"
            6399..6455
                /rpt_family "CTD)n"
            6749..6813
                /rpt_family "CTCCTC"
            complement(6814..6892)
                /rpt_family "R1_MM"
            6901..7025
                /rpt_family "R1_P"
            complement(7122..7223)
                /rpt_family "R1_P"
            7587..7767
                /rpt_family "R1_P"
            7768..8040
                /rpt_family "CGAA)n"
            8289..8368
                /rpt_family "R4A"
            8369..8492
                /rpt_family "R4A"
            8551..8682
                /rpt_family "R1_MM"
            8683..8708
                /rpt_family "AAAA)n"
            complement(8742..8923)
                /rpt_family "RS1M1"
            9162..9247
                /rpt_family "R1_P"
            complement(9692..9743)
                /rpt_family "R4"
            9744..9786
                /rpt_family "CTD)n"

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            repeat_region
                complement(9787..9939)
                /rpt_family "R4"
            repeat_region
                10039..10187
                /rpt_family "Pb1D7"
            repeat_region
                10204..10252
                /rpt_family "CTD)n"
            repeat_region
                complement(10306..10365)
                /rpt_family "R1_P"
            repeat_region
                complement(10514..10855)
                /rpt_family "M11"
            repeat_region
                11080..11276
                /rpt_family "L1M6"
            repeat_region
                11374..11485
                /rpt_family "11485"
            repeat_region
                11489..11672
                /rpt_family "11672"
            repeat_region
                11687..11743
                /rpt_family "11743"
            repeat_region
                12740..12771
                /rpt_family "CTD)n"
            repeat_region
                complement(13217..13335)
                /rpt_family "MER20b"
            repeat_region
                13415..13542
                /rpt_family "CTD)n"
            repeat_region
                complement(13609..14061)
                /rpt_family "MER20b"
            repeat_region
                14008..14346
                /rpt_family "CTD)n"
            repeat_region
                complement(14364..14411)
                /rpt_family "R1_MM"
            repeat_region
                14687..14844
                /rpt_family "R1_MM"
            repeat_region
                15029..15072
                /rpt_family "CTD)n"
            repeat_region
                complement(15081..15170)
                /rpt_family "R1_P"
            repeat_region
                15269..15705
                /rpt_family "CTD)n"
            repeat_region
                15706..15863
                /rpt_family "CTD)n"
            repeat_region
                15983..16043
                /rpt_family "CTD)n"
            repeat_region
                16042..16063
                /rpt_family "CTD)n"
            repeat_region
                complement(16662..16709)
                /rpt_family "CTD)n"
            repeat_region
                16777..17391
                /rpt_family "L2"
            repeat_region
                complement(17441..17543)
                /rpt_family "R1_P"
            repeat_region
                17636..17729
                /rpt_family "L2"
            repeat_region
                17927..18009
                /rpt_family "18009"
            repeat_region
                complement(18071..18253)
                /rpt_family "R2"
            repeat_region
                18290..18372
                /rpt_family "1104"
            repeat_region
                18473..18492
                /rpt_family "R1_MM"
            repeat_region
                21953..21991
                /rpt_family "CTD)n"
            repeat_region
                21991..22033
                /rpt_family "CTD)n"
            repeat_region
                complement(22972..23172)
                /rpt_family "L1M1"
            repeat_region
                23435..23496
                /rpt_family "CTD)n"
            repeat_region
                24770..24871
                /rpt_family "CTD)n"
            repeat_region
                27641..27727
                /rpt_family "CTD)n"
            repeat_region
                28830..28849

```


[illegible][illegible]

